

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 20:02:31 ; Search time 154.23 Seconds
(without alignments)
7193.137 Million cell updates/sec

Title: US-10-081-864A-14
Perfect score: 678
Sequence: 1 atggcccccgcgagaaagc.....gccacacacgtctctctgtaa 678

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655.2	96.6	723	US-10-152-296-1	Sequence 1, Appli
2	438	64.6	678	US-09-459-956-6	Sequence 6, Appli
3	257.4	38.0	699	US-09-459-956-5	Sequence 5, Appli
4	251.8	37.1	720	US-09-839-650-1	Sequence 1, Appli
5	245	36.1	1482	US-09-977-887-1	Sequence 1, Appli
6	216.6	31.9	801	US-09-459-956-7	Sequence 7, Appli
7	144.8	21.4	690	US-09-459-956-2	Sequence 2, Appli
8	119	17.6	1104	US-09-277-716-30	Sequence 30, Appli
9	119	17.6	1104	US-09-609-1618-30	Sequence 30, Appli
10	119	17.6	1279	US-09-277-716-31	Sequence 31, Appli
11	119	17.6	1279	US-09-609-1618-31	Sequence 31, Appli
12	110.4	16.3	696	US-09-459-956-4	Sequence 4, Appli
13	100.2	14.8	717	US-09-214-909-1	Sequence 1, Appli
14	99.2	14.6	696	US-09-459-956-3	Sequence 3, Appli
15	99	14.6	717	US-09-466-241-31	Sequence 31, Appli
16	98.4	14.5	1079	US-09-609-1618-15	Sequence 15, Appli
17	98.4	14.5	1079	US-09-626-581D-64	Sequence 64, Appli
18	98.4	14.5	1079	US-09-415-765B-64	Sequence 64, Appli
19	98.4	14.5	1079	US-09-626-580C-64	Sequence 64, Appli
20	98.4	14.5	1085	US-09-277-716-15	Sequence 15, Appli
21	95.2	14.0	1021	US-09-839-650-2	Sequence 2, Appli
22	94.4	13.9	762	US-08-532-390-40	Sequence 40, Appli
23	94.4	13.9	762	US-08-717-294-40	Sequence 40, Appli
24	93	13.7	720	US-09-172-063-14	Sequence 14, Appli
25	93	13.7	720	US-09-316-919-15	Sequence 15, Appli
26	93	13.7	720	US-09-602-641-14	Sequence 14, Appli
27	93	13.7	720	US-09-316-920A-15	Sequence 15, Appli

28	92.8	13.7	7353	US-08-786-531B-1	Sequence 1, Appli
29	91.4	13.5	717	US-09-513-783A-43	Sequence 43, Appli
30	91.4	13.5	717	US-09-430-656-43	Sequence 43, Appli
31	91.4	13.5	720	US-09-094-359-9	Sequence 9, Appli
32	91.4	13.5	720	US-09-172-063-12	Sequence 12, Appli
33	91.4	13.5	720	US-09-172-063-17	Sequence 17, Appli
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36	91.4	13.5	720	US-09-602-641-12	Sequence 12, Appli
37	91.4	13.5	720	US-09-602-641-17	Sequence 17, Appli
38	91.4	13.5	720	US-09-704-463-9	Sequence 9, Appli
39	91.4	13.5	720	US-09-316-920A-13	Sequence 13, Appli
40	91.4	13.5	720	US-09-316-920A-18	Sequence 18, Appli
41	91.4	13.5	768	US-09-172-063-38	Sequence 28, Appli
42	91.4	13.5	768	US-09-172-063-33	Sequence 33, Appli
43	91.4	13.5	768	US-09-602-641-28	Sequence 28, Appli
44	91.4	13.5	768	US-09-602-641-33	Sequence 33, Appli
45	91.4	13.5	972	US-09-172-063-30	Sequence 30, Appli

ALIGNMENTS

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RESULT 1
US-10-152-296-1
Sequence 1, Application US/10152296
Patent No. 6723537
GENERAL INFORMATION:
APPLICANT: Beele, Beau
TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells
FILE REFERENCE: 021044-000110US
CURRENT APPLICATION NUMBER: US/10152,296
PRIOR FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/291,871
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 723
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:mammalian
OTHER INFORMATION: codon-optimized variant (DSRED) of Discosoma sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(723)
OTHER INFORMATION: DSRED
US-10-152-296-1
Query Match 96.6%; Score 655.2; DB 4; Length 723;
Best Local Similarity 98.1%; Pred. No. 6.8e-125;
Matches 663; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
2 TGCGCTCTCCGAGAACTATCCAGAGTTACGCTTCAAGTGGCATGAGGCA 61
5 TGCCCTCTCCCAAGAGCTATCAAGAGTTACGCTTCAAGTGGCATGAGGCA 64
62 CCGTGAACGGCAGAGTTCAGATCGAGGCGAGGCGAGGCGCCCTTCAAGAGGCGC 121
65 CCGTGAACGGCAGAGTTCAGATCGAGGCGAGGCGAGGCGCCCTTCAAGAGGCGC 124
122 ACAACACCGTGAAGTTGAAGTGACCAAGAGGCGCCCTTCAAGAGGCGC 181
125 ACAACACCGTGAAGTTGAAGTGACCAAGAGGCGCCCTTCAAGAGGCGC 184
182 TGTCCCGCCAGTTCAGTGAAGCTTCAAGAGTTCAGTGAAGGACCCCGGACATCCG 241
185 TGTCCCGCCAGTTCAGTGAAGCTTCAAGAGTTCAGTGAAGGACCCCGGACATCCG 244
242 ACTACAGAAGCTGTCTTCCCGGAGGCTTCAAGTGGAGCGCGTGAATTCGAGG 301
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Db 245 ACTACAGAACTGCTCTCCCGAGGGCTTCAAGTGGAGACGGCTGATGAATTCGAGG 304
Qy 302 AGCGGCGGTGGCCACCGGTGACCCAGAGCTCTCCCTGACAGACGGCTGTTCAATCA 361
Db 305 AGCGGCGGTGGTGAACCGGTGACCCAGAGCTCTCCCTGACAGACGGCTGTTCAATCA 364
Qy 362 AGGTGAAGTTCATGCGGGGTGAATTCCTCCCTCGACGGGCGGCTGATGCAAGAAAGCA 421
Db 365 AGGTGAAGTTCATGCGGGGTGAATTCCTCCCTCGACGGGCGGCTGATGCAAGAAAGCA 424
Qy 422 TGGGCTGGAGGAGCTTCACCGAGCGCTGTACCCCGCGACGGGCTGTGAAGGCGAGA 481
Db 425 TGGGCTGGAGGAGCTTCACCGAGCGCTGTACCCCGCGACGGGCTGTGAAGGCGAGA 484
Qy 482 TCACCAAGGCGCTGAGTGAAGGACGGCGGCTACTACTGTGTGAATTCATCT 541
Db 485 TCACCAAGGCGCTGAGTGAAGGACGGCGGCTACTACTGTGTGAATTCATCT 544
Qy 542 ACATGGCCAGAGAGCGGCTGAGCTGCGGCTACTACTAGTGAACAGAGCTGAGCA 601
Db 545 ACATGGCCAGAGAGCGGCTGAGCTGCGGCTACTACTAGTGAATTCAGCTGAGCA 604
Qy 602 TCACCTCCCAAGAGGAGTACCAATCTGTGAGCAAGTACGAGCGACCGAGGCGCGC 661
Db 605 TCACCTCCCAAGAGGAGTACCAATCTGTGAGCAAGTACGAGCGACCGAGGCGCGC 664
Qy 662 ACCACCTGTTCTCTGA 677
Db 665 ACCACCTGTTCTCTGA 680

RESULT 2

US-09-459-956-6
; Sequence 6, Application US/0945956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsielen, Roger Y.
; APPLICANT: Gonzalez, Iii, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: *Discoosoma* sp
US-09-459-956-6

Query Match 64.6%; Score 438; DB 3; Length 678;
Best Local Similarity 77.9%; Pred. No. 1,4e-80;
Matches 528; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

Qy 1 ATGGGCTCTCCGAGAACTCATCACCGAGTTCAATGCGTTCAAGTGGCGATGAGGCG 60
Db 1 ATGAGGCTCTCCAGAAATGTTATCAAGAGTTCAAGGTTTAAGTTCCGATGGAAGA 60
Qy 61 ACCGTGAACGGCCACGAGTTGAGATGAGGGCGAGGGCGAGGGCGCCCTTACGAGGCG 120
Db 61 ACCGTCAATGGGCGAGGTTGAATGAAAGCGAAGAGAGGGGAGGCGCATAGAGGCG 120
Qy 121 CACAAGACCGTGAAGTGAAGTGAACCAAGGGCGGCGCCCTTCCGCTTGGGAATC 180
Db 121 CACAATACCGTGAAGTGAAGTGAACCAAGGGGAGGCGCTTGGCATTTGGGATATT 180

Qy 181 CTGTCCCCCAGTTCCAGTACGAGCTCCAGAGTGTACGTGAAGCACCCCGCGAGATCCCC 240
Db 181 TTGTACCAACAATTCAGTATGAAAGCAAGGTATATGTCAAGCACCTTGGCAATACCA 240
Qy 241 GACTACAAAGAGTGTCTTCCCGAGAGGCTTCAAGTGGAGCGCGTGAATGAATTCGAG 300
Db 241 GACTATAAAAGCTGTATTTCCGAAAGATTTTAATGGGAAGGCTCATGAACTTTGAA 300
Qy 301 GACGCGCGGTGGCGACCGTGAACCCAGACTCTCTCCCTGACAGAGCGGCTTCAATAC 360
Db 301 GACGCGCGGTGTACTGTGAACCCAGAAATTCAGTTGACAGATGGCTGTTTCATCTAC 360
Qy 361 AAGGTGAAGTTCAATGCGGCGTGAATTCCTCCCGACGGGCGGCGGATGCAAGAGACC 420
Db 361 AAGGTCAAGTTCAATGCGGCGTGAATTCCTCCCGATGACCTGTTATGCAAAAGAGCA 420
Qy 421 ATGGGCTGGAGGAGCTTCACCGAGCGCTGTACCCCGCGACGGCGTGTGAAGGCGAG 480
Db 421 ATGGGCTGGAGGAGCTTCACCGAGCGCTGTATCTGTGATGGCGGTGGAAGAGAG 480
Qy 481 ATCCCAAGGCGCTGAACTGAAGAGACGGCGGCTACTACTGTGTGAAGTTCATCTC 540
Db 481 ATTCATAGGCTGTGAAGCTGAAGAGACGGTGTCTATTACTAGTTGAATTCAAAATATT 540
Qy 541 TACATGGCCAAAGAGCGGCTGAGCTGCGGCTACTACTACGTGAGCACCAAGCTGAGC 600
Db 541 TACATGGCCAAAGAGCGGCTGAGCTGCGGCTACTACTACGTGAGTCTCAAACTGAT 600
Qy 601 ATCACTCCCAAGAGGAGTACCAACCATGTGAGAGTACGAGCGCACCGAGGCGCG 660
Db 601 ATAAAGGAGGAGGAGTATACATGTTGAGGAGATATGAAGAAACGAGGAGCGC 660
Qy 661 CACCACTGTTCTCTGA 678
Db 661 CACCACTGTTCTCTGA 678

RESULT 3

US-09-459-956-5
; Sequence 5, Application US/0945956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsielen, Roger Y.
; APPLICANT: Gonzalez, Iii, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: *Discoosoma striata*
US-09-459-956-5

Query Match 38.0%; Score 257.4; DB 3; Length 699;
Best Local Similarity 62.4%; Pred. No. 9,4e-44;
Matches 421; Conservative 0; Mismatches 251; Indels 3; Gaps 1;

Qy 1 ATGGGCTCTCCGAGAACTCATCACCGAGTTCAATGCGTTCAAGTGGCGATGAGGCG 60
Db 1 ATGAGTGTCTCCAGAGTGTGATCAAGAGAAATGTATCATCTTCAATCTGGAAGA 60
Qy 61 ACCGTGAACGGCCACGAGTTGAGATGAGGGCGAGGGCGAGGGCGCCCTTACGAGGCG 120

Db	122	CCACCATGGGTGTGATTAAACGACATGAAAGATTAAAGCTGAAGATGGAAGAAAATGTAA	181
Oy	68	ACGGCCACAGAGTTGAGAGTCGAGGGCGAGGGCGAGGGCGCCGCTTACGAGGGCCACAAC	127
Db	182	ACGGGCATGCTTTTGTGATTCGAAAGGAAGAAAGAAAGCCTTATCGATGGGACACACA	241
Oy	128	CCGTGAATTGAAGGTGACCAAGGGCGGGCCCCCTTCCTTCGCTGGGACATCTCTGTCC	187
Db	242	CTTTAAACCTGGAAATGGAAGGAGGTGGCCCTCTGCTTTTCTTACGATTCCTGTCAA	301
Oy	188	CCCAATTCACAGTACGGCTCCAAAGGTGACGTGAAGCACCACCGCATCTCCCGACTACA	247
Db	302	AACGCTTCCAGTACGGAAACAGAGCATTTGACAAATATCCCAACGATATATAGCAGCTATT	361
Oy	248	AGAACTGTCTTCCCCCGAGGGCTTCAAAGTGGGAGCGGTATGAACTTCGAGGACGGG	307
Db	362	TCAAGCAATCGTTTCCCGAGGATATTCTCTGGGAAAGAACATGACTTTTGAAGACAAAG	421
Oy	308	GGGTGGCCACCGTGACCCAGGACTCTCCCTGACGAGACGGCTGCTTCACTCAAGGTGA	367
Db	422	GCATTGTCAAAGTGAAGTAAGTACATATAGCATGAGAGAAAGACTCTTTTATCTATGAATTC	481
Oy	368	AGTTCATCGGCGTGAATCTCCCTTCGACGCGCCCGGTGATGAGAAAGAACATGGGCT	427
Db	482	GTTTGTGATGGATGAATCTTCTCCCAATGGTCCGGTATATGCAAAAAAACTTTGAGT	541
Oy	428	GGGAGGCTCCACCGGAGCCCTGTATCCCCCGGACGGCGGTGTGAAGGGCGGATCCACA	487
Db	542	GGGAACCATTCACGTGAGATTATATACGTGCGGTGAGAGTGTCTGTGGAGATATTATAGC	601
Oy	488	AGGCCCTGAACCTGAAGACGAGCGGCGCACTACTCTGGAGTTCAAGTCACTCATGATG	547
Db	602	ATTCTCTGTGTGAGGAGGAGGTGGCCATTACCAATGTATGACTTTCAAAAGTATTTACAAAG	661
Oy	548	CCAAAGAACCCGCTGACGCTGCCCGGCTTACTATGCTGACACCAAGCTGACATCACT	607
Db	662	CAAAAAAAGTTGTCAAATTGCGACACTATCACTTTGTGACCATGCAATTTGAGATCTTGA	721
Oy	608	CCCAACACAGAGACTACACCAATCGTGGAGCACTACGACGACCCGAGGGCGGCA	662
Db	722	ACCATGACAAAGATTTACAAACAAAGTAAACGCTGTATGAAATGCAAGTGTCTGCTTA	776

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RESULT 7
US-09-459-956-2
; Sequence 2, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: OPTICAL METHODS
; CURRENT APPLICATION NUMBER: US/09/459, 956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Anemonia majano
US-09-459-956-2

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Query Match	21.4%	Score 144.8	DB 3	Length 690
Best Local Similarity	52.4%	Pred. No. 8.7e-21		
Matches 345	Conservative 0	Mismatches 307	Indels 6	Gaps 1

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Db 1 ATGGCTCTTTCAACAGATTATCGGAGATGATCATATAATGCTTACATATGATGAGC 60
QY 61 ACCGTGAACGCGCACGAGTTTCAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGCG 120
Db 61 ACCGTGAACGCGCACGAGTTTCAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGCG 120
QY 61 TGTGTCAATGGGCACTTACTTAACGTCAGAGGAGGAGGAGGAGGAGGAGGAGG 120
Db 61 TGTGTCAATGGGCACTTACTTAACGTCAGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CACAAACCGGTGAAGTTGAAGTGAACAGGCG-----GGCCCTTCCCTTCCGCTG 174
Db 121 CACAAACCGGTGAAGTTGAAGTGAACAGGCG-----GGCCCTTCCCTTCCGCTG 174
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Db 121 AGCAGACTCTTCACTTTTAAAGTCACATGCGCCAGCGTGGGCGCCCTTCCATTTCTT 180
QY 175 GACATCTGTCCCGCAGTTCCAGTACGGCTCCAGGTGAAGTGAAGACCCCGCGAC 234
Db 175 GACATCTGTCCCGCAGTTCCAGTACGGCTCCAGGTGAAGTGAAGACCCCGCGAC 234
QY 181 GACATCTGTCTACAGTGTTCATTAATGAAATCGATGCTTTATGCGTATCTTACAT 240
Db 181 GACATCTGTCTACAGTGTTCATTAATGAAATCGATGCTTTATGCGTATCTTACAT 240
QY 235 ATCCCGACTCAAGAGAGCTGTCTTCCCGAGGCGTTCAAGTGGAGCGCGTGAATGA 294
Db 235 ATCCCGACTCAAGAGAGCTGTCTTCCCGAGGCGTTCAAGTGGAGCGCGTGAATGA 294
QY 241 ATGCCGACTATTTTCAACAGAGATTTCTGACGGAATGTCATATGAAAGACTTTTAC 300
Db 241 ATGCCGACTATTTTCAACAGAGATTTCTGACGGAATGTCATATGAAAGACTTTTAC 300
QY 295 TTGAGAGAGCGGCGGTGGCGACCGTGAACCGAGACTCTCCCTGAGAGAGCGCTGCTT 354
Db 295 TTGAGAGAGCGGCGGTGGCGACCGTGAACCGAGACTCTCCCTGAGAGAGCGCTGCTT 354
QY 301 TATGAAGATGAGAGGAGTGTCTACAGCAGTTGGGAAATGAAGCTTTAAAGCACTGCTT 360
Db 301 TATGAAGATGAGAGGAGTGTCTACAGCAGTTGGGAAATGAAGCTTTAAAGCACTGCTT 360
QY 355 ATCTCAAGGTGAAGTTCATGCGCGTGAAGTCTCCCTCCGAGGCGCCCGTGAATGAGA 414
Db 355 ATCTCAAGGTGAAGTTCATGCGCGTGAAGTCTCCCTCCGAGGCGCCCGTGAATGAGA 414
QY 361 GAGCAAAATCCAGCTTTCATGATGAAGTAACTTTCGCTGATGAGACCTGTATGAGGA 420
Db 361 GAGCAAAATCCAGCTTTCATGATGAAGTAACTTTCGCTGATGAGACCTGTATGAGGA 420
QY 415 AAGACCATGGCTGGAGAGGCTTCAACCGAGCGCTGTATCCCGCGACGCGCTGTGAAG 474
Db 415 AAGACCATGGCTGGAGAGGCTTCAACCGAGCGCTGTATCCCGCGACGCGCTGTGAAG 474
QY 421 AAGACAACGTTTGGGAGCCATCTTTGAGAAATGATCTGTGAGATGGAATATTGAAG 480
Db 421 AAGACAACGTTTGGGAGCCATCTTTGAGAAATGATCTGTGAGATGGAATATTGAAG 480
QY 475 GCGGAGATCCAGAGGCGCTGAAGTGAAGAGAGCGGCGGCACTACCTGTGTGAAGTTCA 534
Db 475 GCGGAGATCCAGAGGCGCTGAAGTGAAGAGAGCGGCGGCACTACCTGTGTGAAGTTCA 534
QY 481 GGTGATGTACCGCTTCTCATGTCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 481 GGTGATGTACCGCTTCTCATGTCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 535 TCCATCTCATGAGGCAAGAGCGCGTGCAGCTCCCGGCTACTCATGATGAGACCAAG 594
Db 535 TCCATCTCATGAGGCAAGAGCGCGTGCAGCTCCCGGCTACTCATGATGAGACCAAG 594
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QY 595 CTGACATCATCTCCCAACAGAGGACTACACCATGTGTGAGCAGTACGAGCGCACCG 652
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QY 601 ATTGAGAGGAGCGGAGCTTGAAGAAAGTGGCAACAGTTCACGTACGAGGAGCACCTG 658
Db 601 ATTGAGAGGAGCGGAGCTTGAAGAAAGTGGCAACAGTTCACGTACGAGGAGCACCTG 658

RESULT 8
US-09-277-716-30
; Sequence 30, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; ORGANISM: Ptilosarcus gurneyi
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; FEATURE:
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (Insert A)
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US-09-277-716-30
Query Match 17.6%; Score 119; DB 3; Length 1104;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;
Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

QY 23 TCACGAGTTCATGCGCTTCAAGTGTCCGATGAGAGGAGGAGGAGGAGGAGGAGGAGG 82
Db 23 TCACGAGTTCATGCGCTTCAAGTGTCCGATGAGAGGAGGAGGAGGAGGAGGAGGAGG 82
QY 65 TGAAGAGATTAATGTCGCGCAAGAGCTAGCGTTGAAGAAATGATGAACATACGTTT 124
Db 65 TGAAGAGATTAATGTCGCGCAAGAGCTAGCGTTGAAGAAATGATGAACATACGTTT 124
QY 83 AGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 142
Db 83 AGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 142
QY 125 CCATGAGAGATTTTGAAGAAAGCATATGATTTATTTGAAGAACCAATGATGAAATCCGG 184
Db 125 CCATGAGAGATTTTGAAGAAAGCATATGATTTATTTGAAGAACCAATGATGAAATCCGG 184
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Db 383 ACTTCCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 442
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QY 503 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 562
Db 503 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 562
QY 545 AGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 604
Db 545 AGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 604
QY 563 AGCTGCGGCGCTACATCTACAGTGAACCAAGAGTGAATCACTCCCAACAGAGGAG 622
Db 563 AGCTGCGGCGCTACATCTACAGTGAACCAAGAGTGAATCACTCCCAACAGAGGAG 622
QY 605 AAGAAATTCGGAATATCATCTTATCATCATCTGCTGAGAGAAACCTTACGTGAAGAG 664
Db 605 AAGAAATTCGGAATATCATCTTATCATCATCTGCTGAGAGAAACCTTACGTGAAGAG 664
QY 623 ACACCATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 645
Db 623 ACACCATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 645
QY 665 GAGCTTGTGTGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 687
Db 665 GAGCTTGTGTGAACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 687

RESULT 9
US-09-609-161B-30
; Sequence 30, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; CURRENT APPLICATION NUMBER: US/09/609,161B
; EARLIER FILING DATE: 2000-06-30
; EARLIER APPLICATION NUMBER: 09/277,716
; EARLIER FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 1104
TYPE: DNA
ORGANISM: Ptiliosarcus gurneyi
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..(747)
OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-609-161B-30

Query Match 17.6%; Score 119; DB 3; Length 1104;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;
Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

QY 23 TCACCGAGTTGATGCGCTTCAAGTGGCGCATGAGGGGCAACCGTGAAGTTGAAG 82
DB 65 TGAAGAGATTATGTCGGCAAAAGCTAGCGTTGAAGGATCGTGAACATCACGTTT 124
QY 83 AGATCGAGGGGAGGGGCGCGCCCTACGAGGGCCACAAACCGTGAAGTTGAAG 142
DB 125 CCAATGAGAGATTGTAAGAAAGCAATGATTTTGAAGAACATGATGCAATCCGG 184
QY 143 TGACCAAGGGGCGCGCCCTGCGCTTGGCGCATCTGTCCTCCCGCATTCAGTAC 202
DB 185 TTACAAAGGAGGATCGCTTGCATTCGCTTCGATATGTTCCATAGCTTTCCAAATAC 244
QY 203 GCTCCAGGTGATGTAAGACCCCGCGCATCTCCCGATCAAGAAAGCTGTCCTCC 262
DB 245 GGAATCGCATTTTACGAAATACCAAGACGACATTCGCACTTCTTTCATCATTC 304
QY 263 CCGAGGCTTCAAGTGGAGCGCGGTGATGAACTTGAAGACGCGCGCGTGGACCGTGA 322
DB 305 CGGCTGATTTTCTAGCAAAAGAAATCTACGCTTTGAAGATGGCGCATTTGACATTC 364
QY 323 CCGAGACTCTCTCCCTGAGAGACGGCTGCTTCACTTCAAGTGAAGTTCACTGCGCTGA 382
DB 365 GTTCAGATATTAAGTTTAAAGATGATTAAGTTCCACTCAAAAGTGAAGTAAAGCAACG 424
QY 383 ACTTCCCTCCGAGCGCGCGCTGATGCAAGAAAGACATGGGCTGGAGGCTTCCACCG 442
DB 425 GTTTCCTAGTAAAGGACCGCGTGAACAAAGCCATCTCGCATGAGGCACTGTTTG 484
QY 443 AGCCCTGTATCCCCCGAGCGCGGTGTAAGGGCGAATCCACAAAGCCCTGAAGCTGA 502
DB 485 AGGTGCTTACATGAACAGCGCGCTTCTGTGGGGAAGTATCTGTTTACAACTCG 544
QY 503 AGACGGCGGCGCACTTACCTGTGTGAAGTTCAAGTCACTTACATGCGCAAGAGCCGCTGC 562
DB 545 AGTCAGGAACTATTACTGTGCAACATGAAGAAAGTTTACAGATCCAAAGTGAAGTGA 604
QY 563 AGCTGCCGCTTACATCTAGCTGAGCAACCAAGCTGAGCATCACTCCCAACAGAGACT 622
DB 605 AAGAAATTCGGAATATCACTTATTCATCTGCTGAGAGAAACCTTACGTGAAGAG 664
QY 623 ACACCATGTGAGAGAGTACGAG 645
DB 665 GAAGCTTGTGGAACAACAGAG 687

RESULT 10
US-09-277-716-31
Sequence 31, Application US/09277716A
Patent No. 6232107
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939

EARLIER FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-06-15
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 1279
TYPE: DNA
ORGANISM: Ptiliosarcus gurneyi
FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(720)
OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (insert B)
US-09-277-716-31

Query Match 17.6%; Score 119; DB 3; Length 1279;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;
Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

QY 23 TCACCGAGTTGATGCGCTTCAAGTGGCGCATGAGGGGCAACCGTGAAGTTGAAG 82
DB 38 TGAAGAGATTATGTCGGCAAAAGCTAGCGTTGAAGGATCGTGAACATCACGTTT 97
QY 83 AGATCGAGGGGAGGGGCGCGCCCTACGAGGGCCACAAACCGTGAAGTTGAAG 142
DB 98 CCAATGAGAGATTGTAAGAAAGCAATGATTTTGAAGAACATGATGCAATCCGG 157
QY 143 TGACCAAGGGGCGCGCCCTGCGCTTGGCGCATCTGTCCTCCCGCATTCAGTAC 202
DB 158 TTACAAAGGAGGATCGCTTGCATTCGCTTCGACATTTGTCATAGCTTTCCAAATAC 217
QY 203 GCTCCAGGTGATGTAAGACCCCGCGCATCTCCCGATCAAGAAAGCTGTCCTCC 262
DB 218 GGAATCGCATTTTACGAAATACCAAGACGACATTCGCACTTCTTTCATCATTC 277
QY 263 CCGAGGCTTCAAGTGGAGCGCGGTGATGAACTTGAAGACGCGCGCGTGGACCGTGA 322
DB 278 CGGCTGATTTTCTAGCAAAAGAAATCTACGCTTTGAAGATGGCGCATTTGACATTC 337
QY 323 CCGAGACTCTCTCCCTGAGAGACGGCTGCTTCACTTCAAGTGAAGTTCACTGCGCTGA 382
DB 338 GTTCAGATATTAAGTTTAAAGATGATTAAGTTCCACTCAAAAGTGAAGTAAAGCAACG 397
QY 383 ACTTCCCTCCGAGCGCGCGCTGATGCAAGAAAGACATGGGCTGGAGGCTTCCACCG 442
DB 398 GTTTCCTAGTAAAGGACCGGTGAACAAAGCCATCTCGCATGAGGCACTGTTTG 457
QY 443 AGCCCTGTATCCCCCGAGCGCGGTGTAAGGGCGAATCCACAAAGCCCTGAAGCTGA 502
DB 458 AGGTGCTTACATGAACAGCGCGCTTCTGTGGGGAAGTATCTGTTTACAACTCG 517
QY 503 AGACGGCGGCGCACTTACCTGTGTGAAGTTCAAGTCACTTACATGCGCAAGAGCCGCTGC 562
DB 518 AGTCAGGAACTATTACTGTGCAACATGAAGAAAGTTTACAGATCCAAAGTGAAGTGA 577
QY 563 AGCTGCCGCTTACATCTAGCTGAGCAACCAAGCTGAGCATCACTCCCAACAGAGACT 622
DB 578 AAGAAATTCGGAATATCACTTATTCATCTGCTGAGAGAAACCTTACGTGAAGAG 637
QY 623 ACACCATGTGAGAGAGTACGAG 645
DB 638 GAAGCTTGTGGAACAACAGAG 660

RESULT 11
US-09-609-161B-31
Sequence 31, Application US/09609161B
Patent No. 643682
GENERAL INFORMATION:
APPLICANT: Bryan, Bruce

APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/102,939
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/089,367
PRIOR FILING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/079,624
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 1279
TYPE: DNA
ORGANISM: *Ptilosarcus gurneyi*
FEATURE:
NAME/KEY: CDS
LOCATION: (7)..(720)
OTHER INFORMATION: *Ptilosarcus Green Fluorescent Protein (GFP) (Insert B)*
US-09-609-161B-31

Query Match 17.6%; Score 119; DB 3; Length 1279;
Best Local Similarity 49.4%; Pred. No. 1.7e-15;

Matches 308; Conservative 0; Mismatches 315; Indels 0; Gaps 0;

QY 23 TCACGAGTTCATGCGCTTCAAGTGGCGATGAGGCGACCGTGAACGCGCCAGACTTCG 82
DB 38 TGAAGAGATTATGTCGCGCAAAAGCTAGCGTTGAAGATCGTGAACATCACTGTTTTT 97
QY 83 AGATGAGGCGAGGCGCGCGCGCCCTACGAGGCGCAACACCGTGAAGTTGAAG 142
DB 98 CCAATGAGAGATTGGAAAAGGCAATGTATTTTGAAGAACCAATTGATGCAATCCGG 157
QY 143 TGACCAAGGCGCGCGCGCGCTTCCGCTTGGAGACATCTGTCGCCCGCCAGTTCAGTAC 202
DB 158 TTACAAAGGAGAGTCCGTGCGCATTCGCTTGAACATTTTCCATAGCTTCCAAATAC 217
QY 203 GCTCAAGGTATGCTGAAGCAACCGCGCGCATCCCGCATCAAGAAAGCTGCTTCC 262
DB 218 GGAATCGCACTTTCAGAAATATACCAAGACGATTCGCGCATCTTGTTCATCATTTTC 277
QY 263 CGAGGCGCTTCAAGTGGAGCGCGGTGATGAATTCGAGAGCGCGCGGTGAGACCGTGA 322
DB 278 CGGCTGATTTTTTCTACGAAAGAAATCTAGCTTTGAAGATGCGCCCATTTGTGACATTC 337
QY 333 CCCAGAGCTCTCCCTCGAGAGAGCGCGCTTCTATCTACAGAGTTGATCATCGCGTGA 382
DB 338 GTTCAGATATATAGTTTGAAGATGATTAAGTTCCATCAAAAGTGAAGTAAAGGCAAG 397
QY 383 ACTTCCTCCGAGCGCGCGCGGTGATGAGAGAGACATGGCTGGAGAGGCTTCCACCG 442
DB 398 GTTTCCTAGTAAAGAGCGCGCGGTGATGAGAGAGCGCATCTCGGCGATGAGCGCATGTTG 457
QY 443 AGCGCTGTAACCGCGCGAGCGCGGTGAGAGAGGAGAGTCCAGAGCGCGTGAAGCTGA 502
DB 458 AGTGTCTCAATGAACAGCGCGCGGTGAGAGAGGAGTGAAGTCTCGTTTAAACATTCG 517
QY 503 AGGAGCGCGCGCATCTGATGAGTTCAAGTTCATCTACATGCGCAAGAGCGCGTGC 562
DB 518 AGTGAAGGAGATATTAATCTGTCGCAATGAAAGCTTTTACAGATCCAAAGTGAAGTGA 577
QY 563 AGCTGCGCGGCTACTACTAGTGAAGACCAAGCTGACATCACTTCCCAAGAGAGACT 622
DB 578 AAGAAATCCCGGAAATATCACTTATTCATCATCTGAGAGAAACCTAGTGAAGAG 637
QY 623 AACCATGCTGAGAGCATGACAG 645

DB 638 GAGCTTCGTGAGACACACAG 660

RESULT 12
US-09-459-956-4
Sequence 4, Application US/09459956

Patient No. 6342379

GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.

APPLICANT: Gonzalez, III, Jesus E.

TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY

TITLE OF INVENTION: OPTICAL METHODS

FILE REFERENCE: REGEM1290-4

CURRENT APPLICATION NUMBER: US/09/459,956

CURRENT FILING DATE: 1999-12-13

PRIOR APPLICATION NUMBER: 08/765,860

PRIOR FILING DATE: 1999-05-08

PRIOR APPLICATION NUMBER: 08/481,977

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: PCT/US96/09652

PRIOR FILING DATE: 1996-06-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 696

TYPE: DNA

ORGANISM: *Zoanthus sp*

US-09-459-956-4

Query Match 16.3%; Score 110.4; DB 3; Length 696;
Best Local Similarity 52.5%; Pred. No. 9.1e-14;

Matches 296; Conservative 0; Mismatches 256; Indels 12; Gaps 2;

QY 1 ATGGCTCTCCGAGAACGTATCAACCGATTCATGCGCTTCAAGTGGCGATGAGGCG 60
DB 1 ATGGCTATTTCAAGGACAGTCTAAAGAGAAATGACATGAAATATACATGAGAGG 60
QY 61 ACCGTGAAGCGCCACAGATTTGAGATGAGGCGGAGGCGCGCGCCCTACAGAGGC 120
DB 61 TCCGTCAACGACATTAATTTGTGTATCAGGCGGAGGCGCATTTGATTCGTTCAAGG 120
QY 121 CACAACACCGGAGTGAAGTGAACGAGGCGCGCGCGCTTCCGCTTGGAGCATC 180
DB 121 AAACGACTATTAATCTGTGTATGAGAGAGAGGAGATTTTCACTGAATATCTCAAGACATTA 180
QY 181 CTGTCCCGGAGTTCAGTGAAGGCTCAAGGTATGATGAGAGCAACCGCGCATTCGCC 240
DB 181 TTGTAGTGGCTTAAATAGGAGAGAGAGATTTTCACTGAATATCTCAAGACATTA 240
QY 241 GACTTATTAAGAGCTGTCTTCCCGAGGCTTCAAGTGGAGAGCGGTATGAATTTCCG 300
DB 241 GACTTATTAAGAGCTGTCTTCCCGAGGCTTCAAGTGGAGAGCGGTATGAATTTCCG 300
QY 301 GAGCGCGGCGGAGCGCGGTGACCGAGACTCTCCG-----CAGAGCGGCTTCC 354
DB 301 GATGAGAGAGTCTGATATGAGATGATTAATAGTGAAGTGAAGAGAAATCTGCAAT 360
QY 355 ATCTCAAGAGTGAAGTTCATGAGCGCTGAACTTCCCTCCGAGCGCGCGGTATGAGAG 414
DB 361 TATATTAAGAGCATTTTAATGAGATGAATTTTCTGTGATGAGCTGTATGAGAAAG 420
QY 415 AAGACATGAGGCTGAGAGGCTTCCAGCGAG-----CGCTGTACCGCGGAGCGCGT 468
DB 421 ATGACATTAATCTGGAAGAGATCTGCGAGAAATCATGACATGACATTAAGAGAGGATTA 480
QY 469 CTGAAGGCGGAGATCAAGAGCGCTGAAGCTGAAGAGAGCGCGGCGCATCTGTGTGAG 528
DB 481 CTGAAGGAGAGTGTCTCATGTACTCTTCTGAAGAGATGTGTGGCGTTTACCGGTCAG 540
QY 529 TTCAAGTCACTTACATGAGCAAG 552
DB 541 TTGACACAGTTTACAAAGCAAG 564

RESULT 13
US-09-214-909-1
Sequence 1, Application US/09214909
Patent No. 6486382
GENERAL INFORMATION:
APPLICANT: GORDON-KAMM, WILLIAM
APPLICANT: PIERCE, DOROTHY A.
APPLICANT: BOWEN, BENJAMIN
APPLICANT: BIDNEY, DENNIS
APPLICANT: ROSS, MARGIT
APPLICANT: SCHELONGE, CHRISTOPHER
APPLICANT: MILLER, MICHAEL D.
APPLICANT: SANDAHL, GARY
APPLICANT: MANG, LUTIAN
TITLE OF INVENTION: USE OF THE GREEN FLUORESCENT PROTEIN AS A SCREENABLE
FILE REFERENCE: 033229/0682
CURRENT FILING DATE: 1999-12-20
PRIORITY FILING DATE: 1999-05-01
PRIORITY FILING DATE: 1997-05-01
PRIORITY FILING DATE: 1996-05-01
PRIORITY FILING DATE: 1996-05-01
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 717
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
NAME/KEY: CDS
LOCATION: (1)..(714)
US-09-214-909-1

Query Match 14.8%; Score 100.2; DB 4; Length 717;
Best Local Similarity 50.1%; Pred. No. 1.1e-11;
Matches 336; Conservative 0; Mismatches 323; Indels 12; Gaps 3;

QY 1 ATGGCTCTCTCCGGAACGTCATCACCGAGTTCAATGCGCTTCAAGTGGCGCATGAGAGGC 60
DB 1 ATGTCCAAAGGGCGAGAGCTCTTCAACGGCGGTGGGCCATCTGTGAGACTGAGAGGC 60
QY 61 ACCGTGAACGGCCACGAGTTGAGATGAGAGGCGAGAGGCGCGCCCTTACGAGGCG 120
DB 61 GACGTGAACGGCCACGAGTTCTCGGTGTCCGCGAGAGGCGAGAGGCGAGCCACTACGCGC 120
QY 121 CACAACACCGTGAAGTTGAAGTGACCAAGGCGGCGCCCTCGCCCTTGGGAGATC 180
DB 121 AAGCTCACCTTCAAGTTTATGTGACCA--CCGCAAGCTCCCGTGTGCTTGGCCCAAC 177
QY 181 CTGTCCCCCAGTTCAAGTACGAGCTCAAGGTGTACGTGAAGCACCCCGCCGACAT--- 236
DB 178 CTGTGACACCTTCTCTTACGAGGTGAGTGTCTTCTCAGATACCCCGACCATGAG 237
QY 237 --CCCCGACTCAAGAAAGCTCTTCTCCCGAGGGCTTCAAGTGGAGCGGTATGAG 294
DB 238 CAGACGACCTTCTTCAAGTACGAGCATGCCCCGAGGCTACGTGACGAGAGAACCATCTTC 297
QY 295 TTGAGAGAGCGCGGTGGGACCGGTGACCCGAGGACTCTCTCTGACGAGAGCGGTGCTTC 354
DB 298 TTCAAGAGACGAGCACTACACAGACGAGGCGAGAGTTGAGAGGAGACACCTTC 357
QY 355 ATCTACAAGGTGAAGTTTATCGGCTGAATCTTCCCTTCCAGCGGCGCCGTGATGACAAG 414
DB 358 GTGAACGAGATTGAGCTCAAGGCGATGATTCAAGAGAGAGGCAACATCTCGGCAC 417
QY 415 AAGAGCATGGGTGGAGGCTTCAACGAGGCGCTGTATCCCCCGAGAGGCGGTCTGAG 474
DB 418 AAGCTGAGTACAATCACTACCCACAA--CGTGTATCATCATGCGGACAGACGAGAG 474

RESULT 14
US-09-459-956-3
Sequence 3, Application US/09459956
Patent No. 6342379
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Gonzalez, III, Jesus B.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REG1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
PRIORITY FILING DATE: 1999-12-13
PRIORITY FILING DATE: 1999-05-08
PRIORITY FILING DATE: 1995-06-07
PRIORITY FILING DATE: 1995-06-07
PRIORITY FILING DATE: 1996-06-06
PRIORITY FILING DATE: 1996-06-06
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 696
TYPE: DNA
ORGANISM: Zoanthus sp
US-09-459-956-3

Query Match 14.6%; Score 99.2; DB 3; Length 696;
Best Local Similarity 51.2%; Pred. No. 1.8e-11;
Matches 289; Conservative 0; Mismatches 263; Indels 12; Gaps 2;

QY 1 ATGGCTCTCTCCGGAACGTCATCACCGAGTTCAATGCGCTTCAAGTGGCGCATGAGAGGC 60
DB 1 ATGGCTCAGTCAAGGACGAGTCTTAACAAAGAAATGACATGAAATACCGTATGAGAGG 60
QY 61 ACCGTGAACGGCCACGAGTTGAGATGAGAGGCGAGAGGCGCGCCCTTACGAGGCG 120
DB 61 TGGCTCATATGACATTAATTTGTGATCACGAGAGGCGATTGATATTCGTTCAAGGG 120
QY 121 CACAACACCGTGAAGTTGAAGTGACCAAGGCGGCGCCCTGCGCTTGGCTGGACATC 180
DB 121 AAACAGCTATTAATCTGTGTGTGTGAGAGTGAACATTTGCAATTTGCGAAGACATA 180
QY 181 CTGTCCCCCAGTTCAAGTACGAGCTCAAGGTGTACGTGAAGCACCCCGCCGACATCCC 240
DB 181 TTGTACAGCTGCTTAACTACGAGAAACAGGGTTTCACTGAATATCTTCAAGATGAT 240
QY 241 GACTACAGAAAGCTGTCTTCTCCGAGGCTTCAAGTGGAGAGGCGGTGATGAATCTGAG 300
DB 241 GACTATTTCAAGAACTGTGTCTTCTGATATACATGGAACAGGCTTTTCTTTGAG 300
QY 301 GAGGCGCGGTGGAGACCGTGAACCCAGAGCTCTTCTCTG-----CAGACGCGTGTTC 354
DB 301 GATGAGAGCAATTTGCAATATTAATGAGATATTAACAGTGTGTGAAGAAACTGCATG 360
QY 355 ATCTACAAGGTGAAGTTTATCGGCTGAATCTTCCCTTCCAGAGGCGCCGTGATGACAAG 414

Db 361 TATCATGATGTCATTTTATGAGATGATTTTCTGCTGATGAGACCTGTATGAAAAAG 420
Qy 415 AAGACCATGGGCTGGAGAGGCTTCCACCGAG-----CGCTGTACCCCGCAGCGGCTG 468
Db 421 ATGACAGATTAATCTGGAGGCTCTGCGAGATCATATCCAGTACTTAAGCAGGGGATA 480
Qy 469 CTGAAGGGGAGATCCACAAGGCGCTGAAGCTGAAGAGACGGGCGACACTGATGAGAG 528
Db 481 TTGAAGGGGAGATGCTCTCAATGATCTCTTCTGAAGAGATGGGGGTTTACGGTCCAA 540
Qy 529 TTCAAGTCCATCTACATGAGCCCAAG 552
Db 541 TTCGACACAGTTTACAAAGCAAAAG 564

RESULT 15
US-09-486-241-31

; Sequence 31, Application US/09486241
; Patent No. 6472184
; GENERAL INFORMATION:
; APPLICANT: Hegemann, Peter
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEIC ACID
; TITLE OF INVENTION: POLYMERS
; FILE REFERENCE: 3910/06706
; CURRENT APPLICATION NUMBER: US/09/486,241
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/05219
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: DE19736591.4
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified gene from Aquorea victoria
US-09-486-241-31

Query Match 14.6%; Score 99; DB 4; Length 717;
Best Local Similarity 51.0%; Pred. No. 1.9e-11;
Matches 327; Conservative 0; Mismatches 290; Indels 24; Gaps 3;

Qy 1 ATGCTCTCTCCGAGACGTCATCAACCGAGTTCAATGCGCTTCAAGTGGCGCATGAGAGC 60
Db 1 ATGTCGAAGGGCGAGAGAGCTTTCAACCGGTGTGTCCTCCATCTGTGAGCTGAGACGAC 60
Qy 61 ACCGTGAACGGCGAGAGTTCAGATTCAGAGGGCGAGGGCGCGCCCTTACGAGAGG 120
Db 61 GACGTGAACGGCGAGAGTTCGCGTCTCCGGCGAGGGGTGAAGCGCACTTACGAGC 120
Qy 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTGCGCTGGAGATC 180
Db 121 AAGCTGACCTGTAATTCATCTGACCA---CCGGCAAGCTGCCGCTGGGCCACC 177
Qy 181 CTGTCCCCCGAGTTCCAGTACGGCTTCGAAGTGTACGTGAAGCACCAGCGGACAT--- 236
Db 178 CTGTTCACACCTTCACTACCGTGTGCAAGTGTCTTCCCGCTACCCGACCAACATGAAG 237
Qy 237 ---CCCGACTCAAGAGGTGCTTCCCGAGGGCTTCAAGTGGAGGGCGGTGATGAAC 294
Db 238 CAGCAGAGCTTTTCAAGTCCGCGCAATGCCCGAGGGCTTGTGACAGAGGACCAATCTTC 297
Qy 295 TTGAGAGACGGCGGCGGTGGCGACCGTGAACCCAGACTCTCCCTGACAGACGGCTGCTTC 354
Db 298 TTCAAGAGACGAGCGCACTACAAAGACCGCGCGGATCAAGTTCAGAGGGGACACCTCG 357
Qy 355 ATCTCAAGGTGAAGTTCAATCGCGTGAATCTCCCTCCGAGGCGCCGCTGATGCAAG 414
Db 358 GTGAACCCGATCGAGCTGAAGGGCATTCGCTTCAAGAGAGACGCGCAACATCTCTGGCCAC 417

Qy 415 AAGACCATGGGCTGGAGAGGCTTCCACCGAGGCGCTGTATCCCGCGCAGCGGCTGTGAAG 474
Db 418 AAGCTGAGGTACACTTCAACTCCCAACAGGTGATCATATGCGCCGACAGAGAAAGAC 477
Qy 475 GGCGAGATCCACAAGGCGCTGAGTGAAGACGGCGGCACTACTGCTGAGATT--- 530
Db 478 GGCACTAAGTGAATTCAGATTCGCCCAACAACATGAGAGAGCGGCTCCGTGCAAGCTGGCC 537
Qy 531 -----CAATCATCTACATGAGCCCAAGAGAGCCCGTCAAGTCCCGGCTACTAC 579
Db 538 GACCACTACCAAGCAACACCCCATCGCGATGAGCCCGGTGCTTGTGCGCAACAACAC 597
Qy 580 TACGTGACACCAAGCTGACATCACTTCCCAACAGAGGA 620
Db 598 TACTGTCCACCAAGTCCGCGCTGTCTCAAGAGACCCCAACGA 638

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Job time : 158.23 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2005, 21:06:21 ; Search time 545.658 Seconds

(without alignments)
7628.632 Million cell updates/sec

Title: US-10-081-864a-14

Perfect score: 678
Sequence: 1 atggcctctcccgagaaagt.....gccaccactgtctctgtaa 678Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	678	100.0	678	US-10-006-922-36	Sequence 36, Appl
2	678	100.0	678	US-10-081-864-14	Sequence 14, Appl
3	676.4	99.8	678	US-10-315-920-5	Sequence 5, Appl
4	672.2	99.1	1050	US-10-060-857-7	Sequence 7, Appl
5	670.6	98.9	7495	US-10-742-828-5	Sequence 5, Appl
6	670.2	98.8	675	US-10-006-922-38	Sequence 38, Appl
7	670.2	98.8	675	US-10-081-864-13	Sequence 13, Appl
8	670.2	98.6	747	US-10-785-862-10	Sequence 10, Appl
9	668.4	98.3	678	US-10-315-920-3	Sequence 3, Appl
10	666.4	98.3	7508	US-10-742-828-4	Sequence 4, Appl
11	665.2	98.1	678	US-10-081-864-7	Sequence 7, Appl

12	665.2	98.1	678	US-10-315-920-1	Sequence 1, Appl
13	661.6	97.6	681	US-10-121-258-3	Sequence 3, Appl
14	661.6	97.6	681	US-10-121-258-23	Sequence 23, Appl
15	661.6	97.6	4692	US-10-161-403-29	Sequence 29, Appl
16	661.6	97.6	4692	US-10-433-640-16	Sequence 16, Appl
17	661.6	97.6	6984	US-10-001-189-45	Sequence 45, Appl
18	661.6	97.6	7910	US-10-169-050-20	Sequence 20, Appl
19	661.6	97.6	9320	US-10-471-065-20	Sequence 20, Appl
20	661.6	97.6	9658	US-10-609-019-4	Sequence 4, Appl
21	661.6	97.6	9678	US-10-609-019-3	Sequence 3, Appl
22	661.6	97.6	10263	US-10-609-019-2	Sequence 2, Appl
23	660	97.3	681	US-10-006-922-35	Sequence 35, Appl
24	660	97.3	681	US-10-006-922-37	Sequence 37, Appl
25	660	97.3	5436	US-10-169-050-46	Sequence 46, Appl
26	659.6	97.3	1638	US-10-214-932-51	Sequence 51, Appl
27	659.6	97.3	1647	US-10-214-932-75	Sequence 75, Appl
28	655.2	96.6	723	US-10-152-296-1	Sequence 1, Appl
29	655.2	96.6	723	US-10-739-656-1	Sequence 1, Appl
30	649.8	95.8	678	US-10-121-258-5	Sequence 5, Appl
31	629.6	92.9	681	US-10-121-258-7	Sequence 7, Appl
32	614.2	90.6	681	US-10-311-030-8	Sequence 8, Appl
33	614.2	90.6	713	US-10-311-030-11	Sequence 11, Appl
34	614.2	90.6	713	US-10-311-030-12	Sequence 12, Appl
35	568.6	83.9	675	US-10-724-178-15	Sequence 15, Appl
36	568.6	83.9	678	US-10-121-258-9	Sequence 9, Appl
37	556.4	82.1	678	US-10-006-922-43	Sequence 43, Appl
38	556.4	82.1	678	US-10-081-864-11	Sequence 11, Appl
39	470.6	69.4	549	US-10-724-178-1040	Sequence 1040, Ap
40	459	67.7	501	US-10-724-178-1022	Sequence 1022, Ap
41	438.4	64.7	564	US-10-724-178-1036	Sequence 1036, Ap
42	438	64.6	678	US-09-967-772-6	Sequence 6, Appl
43	438	64.6	678	US-10-006-922-11	Sequence 11, Appl
44	438	64.6	678	US-10-121-258-2	Sequence 2, Appl
45	438	64.6	678	US-10-132-067-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-006-922-36
; Sequence 36, Application US/10006922
; Publication No. US20020197676A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A
; APPLICANT: Fradkov, Arcady F.
; APPLICANT: Labas, Yuliy A.
; APPLICANT: Matz, Mikhail V.
; APPLICANT: Terakikh, Alexey
; TITLE OF INVENTION: No. US20020197676A1el Chromophores/Fluorophores and
; FILE REFERENCE: CLON-035CIP
; CURRENT APPLICATION NUMBER: US/10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/457,898
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,144
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,477
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/457,556
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/444,338
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma species
US-10-006-922-36

Query Match 100.0%; Score 678; DB 13; Length 678;
Best Local Similarity 100.0%; Pred. No. 2e-167;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTCTCTCCGAGAACGTATCAACGAGTTCAATGCGCTTCAAGTCCGATGAGAGGC 60
DB 1 ATGGCTCTCTCCGAGAACGTATCAACGAGTTCAATGCGCTTCAAGTCCGATGAGAGGC 60
QY 61 ACCGTGAACGGCCACAGAGTTGAGATCGAGGCGAGGCGGCGCCCTTACAGAGGC 120
DB 61 ACCGTGAACGGCCACAGAGTTGAGATCGAGGCGAGGCGGCGCCCTTACAGAGGC 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTTGCCTTGGCGTGGACATC 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTTGCCTTGGCGTGGACATC 180
QY 181 CTGTCCCCCAAGTTCCAGTACGGCTCCAAAGGTGTACGTGAAGCACCCCGCAGATCCCC 240
DB 181 CTGTCCCCCAAGTTCCAGTACGGCTCCAAAGGTGTACGTGAAGCACCCCGCAGATCCCC 240
QY 241 GACTACAAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAACTTCCAG 300
DB 241 GACTACAAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAACTTCCAG 300
QY 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCCCTGCAAGAGCGGCTGCTTCACTAC 360
DB 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCCCTGCAAGAGCGGCTGCTTCACTAC 360
QY 361 AAGGTGAAGTTCAATCGCGGTGAACCTTCCCTCCGACGGCGCCCGTGTATGACAGAGAAC 420
DB 361 AAGGTGAAGTTCAATCGCGGTGAACCTTCCCTCCGACGGCGCCCGTGTATGACAGAGAAC 420
QY 421 ATGGGCTGGAGGGCTCCACCGAGGCGCTGTACCCCGCAGCGGCTGTGAAGGGCGAG 480
DB 421 ATGGGCTGGAGGGCTCCACCGAGGCGCTGTACCCCGCAGCGGCTGTGAAGGGCGAG 480
QY 481 ATCCACAAGGCGCTGAGAGCTGAAGGACGCGGCGCACTACTGTGTGAAGTTCAAGTCCATC 540
DB 481 ATCCACAAGGCGCTGAGAGCTGAAGGACGCGGCGCACTACTGTGTGAAGTTCAAGTCCATC 540
QY 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTAGTGAACCAAGCTGAGC 600
DB 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTAGTGAACCAAGCTGAGC 600
QY 601 ATCACTCCCAACAAGAGACTACACATCGTGAAGCAAGTACGAGCGGACCGAGGCGCGC 660
DB 601 ATCACTCCCAACAAGAGACTACACATCGTGAAGCAAGTACGAGCGGACCGAGGCGCGC 660
QY 661 CACCACTGTCTCTGTAA 678
DB 661 CACCACTGTCTCTGTAA 678
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RESULT 2

US-10-081-864-14
; Sequence 14, Application US/10081864
; Publication No. US20030022287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yamshevich, Yuriy
; APPLICANT: Savitsky, Alexander
; APPLICANT: Pradkov, Arady
; TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081, 864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21

NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-14

Query Match 100.0%; Score 678; DB 14; Length 678;
Best Local Similarity 100.0%; Pred. No. 2e-167;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCTCTCTCCGAGAACGTATCAACGAGTTCAATGCGCTTCAAGTCCGATGAGAGGC 60
DB 1 ATGGCTCTCTCCGAGAACGTATCAACGAGTTCAATGCGCTTCAAGTCCGATGAGAGGC 60
QY 61 ACCGTGAACGGCCACAGAGTTGAGATCGAGGCGAGGCGGCGCCCTTACAGAGGC 120
DB 61 ACCGTGAACGGCCACAGAGTTGAGATCGAGGCGAGGCGGCGCCCTTACAGAGGC 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTTGCCTTGGCGTGGACATC 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCGCCCTTGCCTTGGCGTGGACATC 180
QY 181 CTGTCCCCCAAGTTCCAGTACGGCTCCAAAGGTGTACGTGAAGCACCCCGCAGATCCCC 240
DB 181 CTGTCCCCCAAGTTCCAGTACGGCTCCAAAGGTGTACGTGAAGCACCCCGCAGATCCCC 240
QY 241 GACTACAAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAACTTCCAG 300
DB 241 GACTACAAAGAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAACTTCCAG 300
QY 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCCCTGCAAGAGCGGCTGCTTCACTAC 360
DB 301 GACGCGCGCGTGGCGACCGGTGACCCAGGACTCTCCCTGCAAGAGCGGCTGCTTCACTAC 360
QY 361 AAGGTGAAGTTCAATCGCGGTGAACCTTCCCTCCGACGGCGCCCGTGTATGACAGAGAAC 420
DB 361 AAGGTGAAGTTCAATCGCGGTGAACCTTCCCTCCGACGGCGCCCGTGTATGACAGAGAAC 420
QY 421 ATGGGCTGGAGGGCTCCACCGAGGCGCTGTACCCCGCAGCGGCTGTGAAGGGCGAG 480
DB 421 ATGGGCTGGAGGGCTCCACCGAGGCGCTGTACCCCGCAGCGGCTGTGAAGGGCGAG 480
QY 481 ATCCACAAGGCGCTGAGAGCTGAAGGACGCGGCGCACTACTGTGTGAAGTTCAAGTCCATC 540
DB 481 ATCCACAAGGCGCTGAGAGCTGAAGGACGCGGCGCACTACTGTGTGAAGTTCAAGTCCATC 540
QY 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTAGTGAACCAAGCTGAGC 600
DB 541 TACATGGCCAAAGAACCCGTGCAAGCTGCGCGCTTACTACTAGTGAACCAAGCTGAGC 600
QY 601 ATCACTCCCAACAAGAGACTACACATCGTGAAGCAAGTACGAGCGGACCGAGGCGCGC 660
DB 601 ATCACTCCCAACAAGAGACTACACATCGTGAAGCAAGTACGAGCGGACCGAGGCGCGC 660
QY 661 CACCACTGTCTCTGTAA 678
DB 661 CACCACTGTCTCTGTAA 678
```

RESULT 3

US-10-315-920-5
; Sequence 5, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Teresikh, Arady Fedorovich
; APPLICANT: Teresikh, Arady Fedorovich
; TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
; TITLE OF INVENTION: FOR THEIR USE
; FILE REFERENCE: CLON-077CIP

CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant of sequence from Discosoma sp.
US-10-315-920-5

Query Match 99.8%; Score 676.4; DB 16; Length 678;
Best Local Similarity 99.9%; Pred. No. 5,4e-167;
Matches 677; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCTCTCTCGAGAAAGTATCAACCGAGTTCAATGCGCTTCAAGGTGCGCATGAGAGGC 60
Db 1 ATGGCTCTCTCTCGAGAAAGTATCAACCGAGTTCAATGCGCTTCAAGGTGCGCATGAGAGGC 60
QY 61 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGAGGC 120
Db 61 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGAGGC 120
QY 121 CACAACACCGTGAAAGTTGAAGTGAACAAAGGGCGGCGCCCTGCTTGGCTGGAGATC 180
Db 121 CACAACACCGTGAAAGTTGAAGTGAACAAAGGGCGGCGCCCTGCTTGGCTGGAGATC 180
QY 181 CTGTCTCCCGGAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 240
Db 181 CTGTCTCCCGGAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 240
QY 241 GACTACAGAAGAGTGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAATTTCGAG 300
Db 241 GACTACAGAAGAGTGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAATTTCGAG 300
QY 301 GACGCGCGGCTGTGCGACCGGTGAACCGAGATCTCTCTGCAAGACGAGCTGCTTCAATC 360
Db 301 GACGCGCGGCTGTGCGACCGGTGAACCGAGATCTCTCTGCAAGACGAGCTGCTTCAATC 360
QY 361 AAGGTGAAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 420
Db 361 AAGGTGAAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 420
QY 421 ATGGGCTGGAGAGGCTTCAACCGAGGCTGTACCCCGCGAGAGGCTGTGAAGGGCGAG 480
Db 421 ATGGGCTGGAGAGGCTTCAACCGAGGCTGTACCCCGCGAGAGGCTGTGAAGGGCGAG 480
QY 481 ATCCCAAGAGGCTGTGAAGCTGAAGACGAGCGGCGCATCTACTGTGTGAAGTTCAAGTCA 540
Db 481 ATCCCAAGAGGCTGTGAAGCTGAAGACGAGCGGCGCATCTACTGTGTGAAGTTCAAGTCA 540
QY 541 TACATGGCCAGAAAGCCCGTGTGAGTGTGCGGCTTCTACTACTGTGTGAAGACCAAGTGA 600
Db 541 TACATGGCCAGAAAGCCCGTGTGAGTGTGCGGCTTCTACTACTGTGTGAAGACCAAGTGA 600
QY 601 ATCACTCTCCCAAGAGAGACTACACATCTGTGAGAGAGTACGAGCGACCGAGGGCGGC 660
Db 601 ATCACTCTCCCAAGAGAGACTACACATCTGTGAGAGAGTACGAGCGACCGAGGGCGGC 660
QY 661 CACCACTGTTCCTGTAA 678
Db 661 CACCACTGTTCCTGTAA 678

RESULT 4
US-10-060-857-7
Sequence 7, Application US/10060857
Publication No. US20020132318A1

GENERAL INFORMATION:
APPLICANT: Anticancer, Inc.
APPLICANT: Zhao, Ming
APPLICANT: Jiang, Ping
APPLICANT: Xu, Mingxu
APPLICANT: Yang, Meng
TITLE OF INVENTION: IMPROVED FLUORESCENT PROTEINS
FILE REFERENCE: 31276-20032.00
CURRENT APPLICATION NUMBER: US/10/060,857
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: US 60/264,932
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1050
TYPE: DNA
ORGANISM: Coral
US-10-060-857-7

Query Match 99.1%; Score 672.2; DB 13; Length 1050;
Best Local Similarity 99.6%; Pred. No. 6,9e-166;
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCTCTCTCGAGAAAGTATCAACCGAGTTCAATGCGCTTCAAGGTGCGCATGAGAGGC 60
Db 289 ATGGCTCTCTCGAGAAAGTATCAACCGAGTTCAATGCGCTTCAAGGTGCGCATGAGAGGC 348
QY 61 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGAGGC 120
Db 349 ACCGTGAACGGGCGACAGATTGAGATCGAGGGCGAGGGCGAGGGCGGCCCTTACGAGAGGC 408
QY 121 CACAACACCGTGAAAGTTGAAGTGAACAAAGGGCGGCGCCCTGCTTGGCTGGAGATC 180
Db 349 CACAACACCGTGAAAGTTGAAGTGAACAAAGGGCGGCGCCCTGCTTGGCTGGAGATC 408
QY 181 CTGTCTCCCGGAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 240
Db 409 CACAACACCGTGAAAGTTGAAGTGAACAAAGGGCGGCGCCCTGCTTGGCTGGAGATC 468
QY 409 CTGTCTCCCGGAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 240
Db 469 CTGTCTCCCGGAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 528
QY 241 GACTACAGAAGAGTGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAATTTCGAG 300
Db 529 GACTACAGAAGAGTGTCTCTCCCGAGGGGCTTCAAGTGGAGCGGCTGATGAATTTCGAG 588
QY 301 GACGCGCGGCTGTGCGACCGGTGAACCGAGATCTCTCTGCAAGACGAGCTGCTTCAATC 360
Db 589 GACGCGCGGCTGTGCGACCGGTGAACCGAGATCTCTCTGCAAGACGAGCTGCTTCAATC 648
QY 361 AAGGTGAAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 420
Db 649 AAGGTGAAGTTCAATGAGGCTTCAAGGTGTAAGTGAAGACACCCCGCGCATTC 708
QY 421 ATGGGCTGGAGAGGCTTCAACCGAGGCTGTACCCCGCGAGAGGCTGTGAAGGGCGAG 480
Db 709 ATGGGCTGGAGAGGCTTCAACCGAGGCTGTACCCCGCGAGAGGCTGTGAAGGGCGAG 768
QY 481 ATCCCAAGAGGCTGTGAAGCTGAAGACGAGCGGCGCATCTACTGTGTGAAGTTCAAGTCA 540
Db 769 ATCCCAAGAGGCTGTGAAGCTGAAGACGAGCGGCGCATCTACTGTGTGAAGTTCAAGTCA 828
QY 541 TACATGGCCAGAAAGCCCGTGTGAGTGTGCGGCTTCTACTACTGTGTGAAGACCAAGTGA 600
Db 829 TACATGGCCAGAAAGCCCGTGTGAGTGTGCGGCTTCTACTACTGTGTGAAGACCAAGTGA 888
QY 601 ATCACTCTCCCAAGAGAGACTACACATCTGTGAGAGAGTACGAGCGACCGAGGGCGGC 660
Db 889 ATCACTCTCCCAAGAGAGACTACACATCTGTGAGAGAGTACGAGCGACCGAGGGCGGC 948
QY 661 CACCACTGTTCCTGTAA 677
Db 949 CACCACTGTTCCTGTAA 677

DB 421 ATGGGCTGGAGAGCCTCCACCGAGCGCTGTACCCCGGACGCGCTGTGAAGGGCGAG 480
QY 481 ATCCCAAGAGCCCTTGAAAGTGAAGAGCGCGGCCCACTACTGTGTGAAGTTCAAGTCCATC 540
DB 481 ACCCAAGAGCCCTTGAAAGTGAAGAGCGCGGCCCACTACTGTGTGAAGTTCAAGTCCATC 540
QY 541 TACATGGCCCAAGAGAGCCCTGTGAGCTGCGCGGCTACTACTAGTGTGACACCAAGCTGAGC 600
DB 541 TACATGGCCCAAGAGAGCCCTGTGAGCTGCGCGGCTACTACTAGTGTGACACCAAGCTGAGC 600
QY 601 ATCACCCTCCCAAGAGAGCTTACACCATCTGTGAGCACTAGAGCGCAACGAGGCGCGC 660
DB 601 ATCACCCTCCCAAGAGAGCTTACACCATCTGTGAGCACTAGAGCGCAACGAGGCGCGC 660
QY 661 CACCACTGTCTCTG 675
DB 661 CACCACTGTCTCTG 675

RESULT 7

US-10-081-864-13
; Sequence 13, Application US/10081864
; Publication No. US20030022287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Yarushevich, Yuriy
; APPLICANT: Yarushevich, Yuriy
; APPLICANT: Savitsky, Alexander
; APPLICANT: Fradkov, Arcady
; TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
; FILE REFERENCE: C10W-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-13

Query Match 98.8%; Score 670.2; DB 14; Length 675;
Best Local Similarity 99.6%; Pred. No. 2.2e-165;
Matches 672; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGCTCTCTCCGAGAGCTCATCACCGAGTTGATGCGTTCAAGGTGCGATGAGGCG 60
DB 1 ATGGCTCTCTCCGAGAGCTCATCACCGAGTTGATGCGTTCAAGGTGCGATGAGGCG 60
QY 61 ACCGTGAAGCGGCAAGAGTTGAGATGAGAGGCGGAGGCGGCGGCGGCGGCGGCGGCG 120
DB 61 ACCGTGAAGCGGCAAGAGTTGAGATGAGAGGCGGAGGCGGCGGCGGCGGCGGCGGCG 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 181 CTGTCCCGCCAGTTCCAGTACGAGGCTCAAGGTGTAGTGAAGCAACCGCGGCAATCCCC 240
DB 181 CTGTCCCGCCAGTTCCAGTACGAGGCTCAAGGTGTAGTGAAGCAACCGCGGCAATCCCC 240
QY 241 GACTACAAAGAGTGTCTTCCCGGAGGCTTCAATGTGGAGGCGGTGATGAATCTTCGAG 300
DB 241 GACTACAAAGAGTGTCTTCCCGGAGGCTTCAATGTGGAGGCGGTGATGAATCTTCGAG 300
QY 301 GACGGGGGGGTGGAGACCGTGAACCGAGACTCTCTCGTGAAGAGCGGCTGCTCATCTAC 360

DB 301 GACGGGGGGGTGGAGACCGTGAACCGAGACTCTCTCGTGAAGAGCGGCTGCTCATCTAC 360
QY 361 AAGGTGAAGTTCATGTGGCGGTGAATCTTCCCTCCAGCGGCGCGGTGATGCAAGAGACC 420
DB 361 AAGGTGAAGTTCATGTGGCGGTGAATCTTCCCTCCAGCGGCGCGGTGATGCAAGAGACC 420
QY 421 ATGGGCTGGAGAGCCTCCACCGAGGCGCTGTACCCCGGAGGCGGTGTGAAGGGCGAG 480
DB 421 ATGGGCTGGAGAGCCTCCACCGAGGCGCTGTACCCCGGAGGCGGTGTGAAGGGCGAG 480
QY 481 ATCCCAAGAGCCCTTGAAAGTGAAGAGCGCGGCCCACTACTGTGTGAAGTTCAAGTCCATC 540
DB 481 ACCCAAGAGCCCTTGAAAGTGAAGAGCGCGGCCCACTACTGTGTGAAGTTCAAGTCCATC 540
QY 541 TACATGGCCCAAGAGAGCCCTGTGAGCTGCGCGGCTACTACTAGTGTGACACCAAGCTGAGC 600
DB 541 TACATGGCCCAAGAGAGCCCTGTGAGCTGCGCGGCTACTACTAGTGTGACACCAAGCTGAGC 600
QY 601 ATCACCCTCCCAAGAGAGCTTACACCATCTGTGAGCACTAGAGCGCAACGAGGCGCGC 660
DB 601 ATCACCCTCCCAAGAGAGCTTACACCATCTGTGAGCACTAGAGCGCAACGAGGCGCGC 660
QY 661 CACCACTGTCTCTG 675
DB 661 CACCACTGTCTCTG 675

RESULT 8

US-10-785-862-10
; Sequence 10, Application US/10785862
; Publication No. US20040261149A1
; GENERAL INFORMATION:
; APPLICANT: Donald Danforth Plant Science Center
; APPLICANT: Fauquet, Claude M.
; APPLICANT: Padmanabhan, Chellappan
; APPLICANT: Ramachandran, Vantharant
; TITLE OF INVENTION: siRNA-mediated inhibition of gene expression in plant cells
; FILE REFERENCE: C35621/104850
; CURRENT APPLICATION NUMBER: US/10/785,862
; CURRENT FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: the deRed coding sequence
US-10-785-862-10

Query Match 98.8%; Score 670.2; DB 18; Length 747;
Best Local Similarity 99.6%; Pred. No. 2.2e-165;
Matches 672; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGGCTCTCTCCGAGAGCTCATCACCGAGTTGATGCGTTCAAGGTGCGATGAGGCG 60
DB 1 ATGGCTCTCTCCGAGAGCTCATCACCGAGTTGATGCGTTCAAGGTGCGATGAGGCG 60
QY 61 ACCGTGAAGCGGCAAGAGTTGAGATGAGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 120
DB 61 ACCGTGAAGCGGCAAGAGTTGAGATGAGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 120
QY 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 121 CACAACACCGTGAAGTTGAAGGTGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 181 CTGTCCCGCCAGTTCCAGTACGAGGCTCAAGGTGTAGTGAAGCAACCGCGGCAATCCCC 240
DB 181 CTGTCCCGCCAGTTCCAGTACGAGGCTCAAGGTGTAGTGAAGCAACCGCGGCAATCCCC 240
QY 241 GACTACAAAGAGTGTCTTCCCGGAGGCTTCAAGGTGGAGCGGCTGATGAATCTTCGAG 300

Db 241 GACTACAAGAAGCTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
Qy 301 GACGGCGCGCTGGGAGCCGTGACCCAGAGATCTTCCCTGACAGAGCGGTGCTTCACTAC 360
Db 301 GACGCGCGCTGGGAGCCGTGACCCAGAGATCTTCCCTGACAGAGCGGTGCTTCACTAC 360
Qy 361 AAGGTGAAGTTCATCGGCGTGAATCTTCCCTCCGACGCGCCCGTGAATCAGAGAAGACC 420
Db 361 AAGGTGAAGTTCATCGGCGTGAATCTTCCCTCCGACGCGCCCGTGAATCAGAGAAGACC 420
Qy 421 ATGGGCTGGAGGCGCTCCACCGAGCGCTGTACCCCGCGACGCGGTGCTGAAGGGCGAG 480
Db 421 ATGGGCTGGAGGCGCTCCACCGAGCGCTGTACCCCGCGACGCGGTGCTGAAGGGCGAG 480
Qy 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGGAGTTCAAGTCATC 540
Db 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGGAGTTCAAGTCATC 540
Qy 541 TACATGGCCAAAGAGCCCGTGCAGCTGCCGCGCTACTACTAGTGAACCAAGCTGAGC 600
Db 541 TACATGGCCAAAGAGCCCGTGCAGCTGCCGCGCTACTACTAGTGAACCAAGCTGAGC 600
Qy 601 ATCACTCTCCCAACAGAGACTACCACTGTGAGAGCTACAGCGCAACGAGGCGCC 660
Db 601 ATCACTCTCCCAACAGAGACTACCACTGTGAGAGCTACAGCGCAACGAGGCGCC 660
Qy 661 CACCACTGTTCCTG 675
Db 661 CACCACTGTTCCTG 675

RESULT 9

US-10-315-920-3
; Sequence 3, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Fradkov, Arcady Fedorovich
; APPLICANT: Tersikh, Alexey
; TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
; TITLE OF INVENTION: FOR THEIR USE
; FILE REFERENCE: CLON-077CIP
; CURRENT APPLICATION NUMBER: US/10/315, 920
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/211,607
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US01/19097
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant of sequence from Discosoma sp.
; US-10-315-920-3

Query Match 98.6%; Score 668.4; DB 16; Length 678;
Best Local Similarity 99.1%; Pred. No. 6.6e-165;
Matches 672; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGCTCTCTCCGAAAGTTCATCAACGATTCAGTTCCTTCAAGTTCGATGAGAGGC 60
Db 1 ATGGCTCTCTCCGAAAGTTCATCAACGATTCAGTTCCTTCAAGTTCGATGAGAGGC 60
Qy 61 ACCGTGAACGGCCACGAGTTCGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 120
Db 61 ACCGTGAACGGCCACGAGTTCGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 120
Qy 121 CACAAACCGTGAAGTGAAGGTGACCAAGGGCGGGCCCGCTTCGCTTGAGATC 180
Db 121 CACAAACCGTGAAGTGAAGGTGACCAAGGGCGGGCCCGCTTCGCTTGAGATC 180

Qy 181 CTGTCCCCAGTTCACGTAAGGCTCCAGAGGTGATGAGACACCCCGCGACATCCC 240
Db 181 CTGTCCCCAGTTCACGTAAGGCTCCAGAGGTGATGAGACACCCCGCGACATCCC 240
Qy 241 GACTACAAGAACTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
Db 241 GACTACAAGAACTGTCTTCCCGAGGGCTTCAAGTGGAGCGGTGATGAATTCGAG 300
Qy 301 GAGGCGCGCTGGGAGCCGTGACCCAGAGATCTTCCCTCCGACGCGCGGTGCTTATC 360
Db 301 GAGGCGCGCTGGGAGCCGTGACCCAGAGATCTTCCCTCCGACGCGCGGTGCTTATC 360
Qy 361 AAGGTGAAGTTCATCGGCGTGAATCTTCCCTCCGACGCGCCCGTGAATCAGAGAAGACC 420
Db 361 AAGGTGAAGTTCATCGGCGTGAATCTTCCCTCCGACGCGCCCGTGAATCAGAGAAGACC 420
Qy 421 ATGGGCTGGAGGCGCTCCACCGAGCGCTGTACCCCGCGACGCGGTGCTGAAGGGCGAG 480
Db 421 ATGGGCTGGAGGCGCTCCACCGAGCGCTGTACCCCGCGACGCGGTGCTGAAGGGCGAG 480
Qy 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGGAGTTCAAGTCATC 540
Db 481 ATCCACAAGGCGCTGAAGCTGAAGGAGCGGCGCACTACCTGTGGAGTTCAAGTCATC 540
Qy 541 TACATGGCCAAAGAGCCCGTGCAGCTGCCGCGCTACTACTAGTGAACCAAGCTGAGC 600
Db 541 TACATGGCCAAAGAGCCCGTGCAGCTGCCGCGCTACTACTAGTGAACCAAGCTGAGC 600
Qy 601 ATCACTCTCCCAACAGAGACTACCACTGTGAGAGCTACAGCGCAACGAGGCGCC 660
Db 601 ATCACTCTCCCAACAGAGACTACCACTGTGAGAGCTACAGCGCAACGAGGCGCC 660
Qy 661 CACCACTGTTCCTGTA 678
Db 661 CACCACTGTTCCTGTA 678

RESULT 10

US-10-742-828-4
; Sequence 4, Application US/10742828
; Publication No. US20040157294A1
; GENERAL INFORMATION:
; APPLICANT: Heyn, Gisi
; APPLICANT: Heinrich, Gerhard
; TITLE OF INVENTION: TRANSGENIC SCREEN AND METHOD FOR SCREENING MODULATORS OF BRAIN-DE
; TITLE OF INVENTION: TRANSGENIC SCREEN AND METHOD FOR SCREENING MODULATORS OF BRAIN-DE
; FILE REFERENCE: US 1353/03 (VA)
; CURRENT APPLICATION NUMBER: US/10/742, 828
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 10/306, 737
; PRIOR FILING DATE: 2002-11-29
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 4
; LENGTH: 7508
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Unsure
; LOCATION:
; OTHER INFORMATION: Synthesized
; US-10-742-828-4

Query Match 98.3%; Score 666.4; DB 18; Length 7508;
Best Local Similarity 99.1%; Pred. No. 2.5e-164;
Matches 670; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 TGGCTCTCTCCGAAAGTTCATCAACGATTCAGTTCCTTCAAGTTCGATGAGAGGCA 61
Db 2124 TGGCTCTCTCCGAAAGTTCATCAACGATTCAGTTCCTTCAAGTTCGATGAGAGGCA 2183
Qy 62 CCGTGAACGGCCACGAGTTCGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 121
Db 2184 CCGTGAACGGCCACGAGTTCGAGATGAGGGCGAGGGCGCGCCCTTACGAGGGC 2243

QY 122 ACAACACGCTGAGTTGAAGTGAACCAAGGCGGCCCCCTGCTTCCCTGGAGCATCC 181
DB 2244 ACAACACGCTGAGTTGAAGTGAACCAAGGCGGCCCCCTGCTTCCCTGGAGCATCC 2303
QY 182 TGTCCCTCCAGTTCCAGTACGAGCTCCAGAGTGTACGTGAAGCAACCCCGCCGACATCCCG 241
DB 2304 TGTCCCTCCAGTTCCAGTACGAGCTCCAGAGTGTACGTGAAGCAACCCCGCCGACATCCCG 2363
QY 242 ACTACAGAGAGTGTCTTCTTCCCGAGAGGCTTCAAGTGGAGAGCGGTGATGAACCTTCGAG 301
DB 2364 ACTACAGAGAGTGTCTTCTTCCCGAGAGGCTTCAAGTGGAGAGCGGTGATGAACCTTCGAG 2423
QY 302 ACGGCGGCGTGGCGACCGGTGACCCAGAGCTCTCCCTGAGAGAGCGGTCTTCATCTACA 361
DB 2424 ACGGCGGCGTGGCGACCGGTGACCCAGAGCTCTCCCTGAGAGAGCGGTCTTCATCTACA 2483
QY 362 AAGTGAAGTTCAATCGGCGGTGAACCTTCCCTCCGACGCGCCCGTGTATGCAAGAGAACCA 421
DB 2484 AAGTGAAGTTCAATCGGCGGTGAACCTTCCCTCCGACGCGCCCGTGTATGCAAGAGAACCA 2543
QY 422 TGGGCTGGAGAGGCTTCCACCGAGCGCTGTACCCCGCGACGCGGTGTGAAGGCGGAGA 481
DB 2544 TGGGCTGGAGAGGCTTCCACCGAGCGCTGTACCCCGCGACGCGGTGTGAAGGCGGAGA 2603
QY 482 TCCACAGGCGCTGAGCTGAAGAGAGAGCGGCGCACTACCTGTGTGAGATTCAAGTCATCT 541
DB 2604 TCCACAGGCGCTGAGCTGAAGAGAGAGCGGCGCACTACCTGTGTGAGATTCAAGTCATCT 2663
QY 542 ACATGCGCCAGAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAGCA 601
DB 2664 ACATGCGCCAGAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAGCA 2723
QY 602 TACCTCTCCCAACAGAGACTACACCATGTGTGAGAGAGAGCGGCAACCGAGGCGCGC 661
DB 2724 TACCTCTCCCAACAGAGACTACACCATGTGTGAGAGAGAGCGGCAACCGAGGCGCGC 2783
QY 662 ACCACTGTCTCTGTA 677
DB 2784 ACCACTGTCTCTGTA 2799

RESULT 11
US-10-081-864-7
; Sequence 7, Application US/10081864
; Publication No. US2003002287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yarushevich, Yuriy
; APPLICANT: Savitsky, Alexander
; APPLICANT: Fradkov, Arcady
; TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp
US-10-081-864-7

Query Match 98.1%; Score 665.2; DB 14; Length 678;
Best Local Similarity 98.8%; Pred. No. 4.5e-164;
Matches 670; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ATGGCTCTCCGAGAACGTCATCAACGATTGATGCGCTTCAAGGTGCGCATGAGAGGCG 60

DB 1 ATGGCTCTCTCCGAGAACGTCATCAACGATTGATGCGCTTCAAGGTGCGCATGAGAGGCG 60
QY 61 ACCGTGAACCGGCAACGAGTTGAGATCGAGGCGGAGGCGGAGGCGGCGCTTCAACAGAGGCG 120
DB 61 ACCGTGAACCGGCAACGAGTTGAGATCGAGGCGGAGGCGGAGGCGGCGCTTCAACAGAGGCG 120
QY 121 CACACACCGTGAAGTTGAAGGTGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 121 CACACACCGTGAAGTTGAAGGTGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 181 CTGTCCCTCCAGTTCCAGTACGAGCTCCAGAGTGTACGTGAAGCAACCCCGCCGACATCCCG 240
DB 181 CTGTCCCTCCAGTTCCAGTACGAGCTCCAGAGTGTACGTGAAGCAACCCCGCCGACATCCCG 240
QY 241 GACTACAGAGAGCTGTCTTCTTCCCGAGAGGCTTCAAGTGGAGAGCGGTGATGAACCTTCGAG 300
DB 241 GACTACAGAGAGCTGTCTTCTTCCCGAGAGGCTTCAAGTGGAGAGCGGTGATGAACCTTCGAG 300
QY 301 GACGCGGCGGTGGGAGCGGTGACCCAGAGCTCTCCCTGCAAGAGCGGCTTCATCTAC 360
DB 301 GACGCGGCGGTGGGAGCGGTGACCCAGAGCTCTCCCTGCAAGAGCGGCTTCATCTAC 360
QY 361 AAGTGAAGTTCAATCGGCGGTGAACCTTCCCTCCGACGCGCCCGTGTATGCAAGAGAACCA 420
DB 361 AAGTGAAGTTCAATCGGCGGTGAACCTTCCCTCCGACGCGCCCGTGTATGCAAGAGAACCA 420
QY 421 ATGGCTGGAGAGGCTTCCACCGAGCGCTGTACCCCGCGACAGGCGGTGTGAAGGCGGAG 480
DB 421 ATGGCTGGAGAGGCTTCCACCGAGCGCTGTACCCCGCGACAGGCGGTGTGAAGGCGGAG 480
QY 481 ATCCACAGAGCGCTGAGCTGAAGAGAGCGGCGCACTACCTGTGTGAGATTCAAGTCATCT 540
DB 481 ATCCACAGAGCGCTGAGCTGAAGAGAGCGGCGCACTACCTGTGTGAGATTCAAGTCATCT 540
QY 541 TACATGCGCCAGAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAGC 600
DB 541 TACATGCGCCAGAGAGCGCGTGCAGCTGCCGCGTACTACTACGTGAGCAACCAAGCTGAGC 600
QY 601 ATCACTCTCCCAACAGAGACTACACCATGTGTGAGAGAGAGCGGCAACCGAGGCGCGC 660
DB 601 ATCACTCTCCCAACAGAGACTACACCATGTGTGAGAGAGAGCGGCAACCGAGGCGCGC 660
QY 661 CACCACTGTCTCTGTA 678
DB 661 CACCACTGTCTCTGTA 678

RESULT 12
US-10-315-920-1
; Sequence 1, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Fradkov, Arcady Fedorovich
; APPLICANT: Terelikh, Alexey
; TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
; FILE REFERENCE: CLON-077CIP
; CURRENT APPLICATION NUMBER: US/10/315,920
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/211,607
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US01/19097
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant of sequence from Discosoma sp.
US-10-315-920-1

Query Match 98.1%; Score 665.2; DB 16; Length 678;
Best Local Similarity 98.8%; Pred. No. 4.5e-164;
Matches 670; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
QY 1 ATGGCTCTCTCCGAGAACGTATCAACGAGTTTCATGCGCTTCAAGTGCATGAGAGGC 60
DB 1 ATGGCTCTCTCCGAGAACGTATCAACGAGTTTCATGCGCTTCAAGTGCATGAGAGGC 60
QY 61 ACCGGAACCGGCAACGATTCGATCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 120
DB 61 ACCGGAACCGGCAACGATTCGATCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 120
QY 121 CACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGAGATC 180
DB 121 CACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGAGATC 180
QY 181 CTGTCCCTCCGAGTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
DB 181 CTGTCCCTCCGAGTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 240
QY 241 GACTACAAAGAGCTGCTTCCCGAGGGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
DB 241 GACTACAAAGAGCTGCTTCCCGAGGGCTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
QY 301 GACGCGCGGCTGAGGAGCGGAGCCGAGGAGCTTCTCCGAGAGAGCGGCTTCAATC 360
DB 301 GACGCGCGGCTGAGGAGCGGAGCCGAGGAGCTTCTCCGAGAGAGCGGCTTCAATC 360
QY 361 AAGGTGAAGTTCAATCGGCGTGAAGTCTCCCTCCGAGGCGCCCGTGAATCAAGAGAGC 420
DB 361 AAGGTGAAGTTCAATCGGCGTGAAGTCTCCCTCCGAGGCGCCCGTGAATCAAGAGAGC 420
QY 421 ATGGCTGAGGAGGCTTCCAGGAGCGGCTTCAAGGAGCGGCTTCAAGGAGCGGAG 480
DB 421 ATGGCTGAGGAGGCTTCCAGGAGCGGCTTCAAGGAGCGGCTTCAAGGAGCGGAG 480
QY 481 ATTCACAAGGCGCTGAGAGCTGAAGAGCGGCGGAGCTTCTGAGAGTTCAGTCAATC 540
DB 481 ATTCACAAGGCGCTGAGAGCTGAAGAGCGGCGGAGCTTCTGAGAGTTCAGTCAATC 540
QY 541 TACATGCGCAAGAACCCGTCGAGCTGCGGCTTCAATGTAAGTGAAGTGAAGTGAAG 600
DB 541 TACATGCGCAAGAACCCGTCGAGCTGCGGCTTCAATGTAAGTGAAGTGAAGTGAAG 600
QY 601 ATCACTCTCCCAACGAGAGTACACCATCGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
DB 601 ATCACTCTCCCAACGAGAGTACACCATCGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
QY 661 CACCACTGTTCTGTAA 678
DB 661 CACCACTGTTCTGTAA 678
```

RESULT 13
US-10-121-258-3
; Sequence 3, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; FILE REFERENCE: UC083.1CP2CPI
; CURRENT APPLICATION NUMBER: US/10/121.258
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: nucleotide sequence encoding DsRed with mammalian
; OTHER INFORMATION: codon usage
US-10-121-258-3

Query Match 97.6%; Score 661.6; DB 14; Length 681;
Best Local Similarity 98.7%; Pred. No. 3.9e-163;
Matches 667; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
QY 2 TGCGCTCTCCGAGAACGTATCAACGAGTTTCATGCGCTTCAAGTGCATGAGAGGC 61
DB 5 TGCGCTCTCCGAGAACGTATCAACGAGTTTCATGCGCTTCAAGTGCATGAGAGGC 64
QY 62 CCGTGAACGCGCAAGATTCGATCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 121
DB 62 CCGTGAACGCGCAAGATTCGATCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 124
QY 65 CCGTGAACGCGCAAGATTCGATCGAGGGCGAGGGCGGCGCCCTTACAGAGGC 124
DB 122 ACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGAGATC 181
QY 125 ACAACACCGTGAAGTTGAAGTGAACCAAGGGCGGCGCCCTTGCCTTGGAGATC 184
DB 182 TGTCCCTCCGAGTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 241
QY 185 TGTCCCTCCGAGTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 244
DB 242 ACTCAAGAGAGTCTTCTTCCCGAGGGCTTCAAGTGAAGTGAAGTGAAGTGAAGT 301
QY 245 ACTCAAGAGAGTCTTCTTCCCGAGGGCTTCAAGTGAAGTGAAGTGAAGTGAAGT 304
DB 302 ACGGCGGCTGAGGAGCGGAGCCGAGGAGCTTCTCCGAGAGAGCGGCTTCAATC 361
QY 305 ACGGCGGCTGAGGAGCGGAGCCGAGGAGCTTCTCCGAGAGAGCGGCTTCAATC 364
DB 362 AAGTGAAGTTCAATCGGCGTGAAGTCTCCCTCCGAGGCGCCCGTGAATCAAGAGAGC 421
QY 365 AAGTGAAGTTCAATCGGCGTGAAGTCTCCCTCCGAGGCGCCCGTGAATCAAGAGAGC 424
DB 422 TGGGCTGAGAGGCTTCCAGGAGCGGCTTGAAGTGAAGTGAAGTGAAGTGAAGT 481
QY 425 TGGGCTGAGAGGCTTCCAGGAGCGGCTTGAAGTGAAGTGAAGTGAAGTGAAGT 484
DB 482 TCCACAAGGCGCTGAGAGCTGAAGAGCGGCGGAGCTTCTGAGAGTTCAGTCAATC 541
QY 485 TCCACAAGGCGCTGAGAGCTGAAGAGCGGCGGAGCTTCTGAGAGTTCAGTCAATC 544
DB 542 ACATGCGCAAGAACCCGTCGAGCTGCGGCTTCAATGTAAGTGAAGTGAAGTGAAG 601
QY 545 ACATGCGCAAGAACCCGTCGAGCTGCGGCTTCAATGTAAGTGAAGTGAAGTGAAG 604
DB 602 TCACCTCTCCCAACGAGAGTACACCATCGTGAAGTGAAGTGAAGTGAAGTGAAGT 661
QY 605 TCACCTCTCCCAACGAGAGTACACCATCGTGAAGTGAAGTGAAGTGAAGTGAAGT 664
DB 662 ACCACTGTTCTGTAA 677
QY 665 ACCACTGTTCTGTAA 680
```

RESULT 14
US-10-121-258-23
; Sequence 23, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; FILE REFERENCE: UC083.1CP2CPI
; CURRENT APPLICATION NUMBER: US/10/121.258
; PRIOR FILING DATE: 2002-04-10

```

; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence encoding Dered with mammalian
; OTHER INFORMATION: codon usage
US-10-121-258-23

Query Match          97.6%; Score 661.6; DB 14; Length 681;
Best Local Similarity 98.7%; Pred. No. 3.9e-163;
Matches 667; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGGCCCTCCCGAAGCGTCAACCGAGTTGCTTCAAGGTGGCGCATGGAGGGA 61
DB 5 TCGCTCTCCCAAGAACTGATCAAGAGATTCATGCGTTCAAGGTGGCGCATGGAGGGA 64
QY 62 CCGTGAACGGCCACGAGTTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGGCC 121
DB 65 CCGTGAACGGCCACGAGTTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGGCC 124
QY 122 ACAACACCGTGAAGTTGAAGTGACCAAGGCGCGCCCTTGCCTTGCCTGGGACATCC 181
DB 125 ACAACACCGTGAAGTTGAAGTGACCAAGGCGCGCCCTTGCCTTGCCTGGGACATCC 184
QY 182 TGTCCCCCAAGTTCCAGTACGGCTCCAGGTGTGATGTAAGCAACCCCGCGCATCTCCCG 241
DB 185 TGTCCCCCAAGTTCCAGTACGGCTCCAGGTGTGATGTAAGCAACCCCGCGCATCTCCCG 244
QY 242 ACTAAGAAGCTGTCTTCCCCGAGGGCTTCAAGTGGAGGCGCGTGAATGAACTTCAAG 301
DB 245 ACTAAGAAGCTGTCTTCCCCGAGGGCTTCAAGTGGAGGCGCGTGAATGAACTTCAAG 304
QY 302 ACGGCGGCGTGGCGACCGTGACCCAGAGACTCTCTCTGTGAGAGCGGCTGCTTCACTTACA 361
DB 305 ACGGCGGCGTGGCGACCGTGACCCAGAGACTCTCTCTGTGAGAGCGGCTGCTTCACTTACA 364
QY 362 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCCCGTGAATGCAAGAAAGCA 421
DB 365 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCCCGTGAATGCAAGAAAGCA 424
QY 422 TGGGCTGGAGGCGCTTCCACCGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAGA 481
DB 425 TGGGCTGGAGGCGCTTCCACCGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAGA 484
QY 482 TTCACAAGGCGCTGTAAGGTGAAGAGAGCGGCGCACTACTGTGTGAGATTCAAGTCCATCT 541
DB 485 TTCACAAGGCGCTGTAAGGTGAAGAGAGCGGCGCACTACTGTGTGAGATTCAAGTCCATCT 544
QY 542 ACATGGCCCAAGAAAGCCCGTGCAGCTGCCCGGCTACTACTAAGTGAACAACAAGCTGGANA 601
DB 545 ACATGGCCCAAGAAAGCCCGTGCAGCTGCCCGGCTACTACTAAGTGAACAACAAGCTGGANA 604
QY 602 TCACCTCCCAACAAGAGACTACACCATGTGAGAGAGTACGACCGACCGAGGGCGGCC 661
DB 605 TCACCTCCCAACAAGAGACTACACCATGTGAGAGAGTACGACCGACCGAGGGCGGCC 664
QY 662 ACCACCTGTTCTCTGTA 677
DB 665 ACCACCTGTTCTCTGTA 680

RESULT 15
US-10-161-403-29
; Sequence 29, Application US/10161403
; Publication No. US20030119104A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindendaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420
; CURRENT APPLICATION NUMBER: US/10/161,403
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 4692
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBSred1-N1 plasmid from Clontech
US-10-161-403-29

Query Match          97.6%; Score 661.6; DB 15; Length 4692;
Best Local Similarity 98.7%; Pred. No. 4.4e-163;
Matches 667; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TGGCCCTCCCGAAGCGTCAACCGAGTTGCTTCAAGGTGGCGCATGGAGGGA 61
DB 683 TCGCTCTCCCAAGAACTGATCAAGAGATTCATGCGTTCAAGGTGGCGCATGGAGGGA 742
QY 62 CCGTGAACGGCCACGAGTTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGGCC 121
DB 743 CCGTGAACGGCCACGAGTTGAGATCGAGGCGAGGCGAGGCGCCCTTACGAGGGCC 802
QY 122 ACAACACCGTGAAGTTGAAGTGACCAAGGCGCGCCCTTGCCTTGCCTGGGACATCC 181
DB 803 ACAACACCGTGAAGTTGAAGTGACCAAGGCGCGCCCTTGCCTTGCCTGGGACATCC 862
QY 182 TGTCCCCCAAGTTCCAGTACGGCTCCAGGTGTGATGTAAGCAACCCCGCGCATCTCCCG 241
DB 863 TGTCCCCCAAGTTCCAGTACGGCTCCAGGTGTGATGTAAGCAACCCCGCGCATCTCCCG 244
QY 242 ACTAAGAAGCTGTCTTCCCCGAGGGCTTCAAGTGGAGGCGCGTGAATGAACTTCAAG 301
DB 922 ACTAAGAAGCTGTCTTCCCCGAGGGCTTCAAGTGGAGGCGCGTGAATGAACTTCAAG 361
QY 302 ACGGCGGCGTGGCGACCGTGACCCAGAGACTCTCTCTGTGAGAGCGGCTGCTTCACTTACA 361
DB 983 ACGGCGGCGTGGCGACCGTGACCCAGAGACTCTCTCTGTGAGAGCGGCTGCTTCACTTACA 1042
QY 1043 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCCCGTGAATGCAAGAAAGCA 421
DB 1043 AGGTGAAGTTCAATCGGCGTGAATCTTCCCTCCGAGCGGCCCGTGAATGCAAGAAAGCA 1102
QY 1103 TGGGCTGGAGGCGCTTCCACCGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAGA 481
DB 1103 TGGGCTGGAGGCGCTTCCACCGAGCGGCTGTACCCCGCGAGCGGCTGTGAAGGGCGAGA 484
QY 482 TTCACAAGGCGCTGTAAGGTGAAGAGAGCGGCGCACTACTGTGTGAGATTCAAGTCCATCT 541
DB 482 TTCACAAGGCGCTGTAAGGTGAAGAGAGCGGCGCACTACTGTGTGAGATTCAAGTCCATCT 541
QY 542 ACATGGCCCAAGAAAGCCCGTGCAGCTGCCCGGCTACTACTAAGTGAACAACAAGCTGGANA 601
DB 1223 ACATGGCCCAAGAAAGCCCGTGCAGCTGCCCGGCTACTACTAAGTGAACAACAAGCTGGANA 1282
QY 602 TCACCTCCCAACAAGAGACTACACCATGTGAGAGAGTACGAGCGACCGAGGGCGGCC 661
DB 1283 TCACCTCCCAACAAGAGACTACACCATGTGAGAGAGTACGAGCGACCGAGGGCGGCC 1342
```

QY 662 ACCACTGTCTCTGA 677
| | | | | | | | | |
Db 1343 ACCACTGTCTCTGA 1358

Search completed: May 29, 2005, 23:53:07
Job time : 549.658 secs

Db 298 TTGAGAGAGGGGGCGCTGTGTGACCGTGAACCCAGACTTCTCTCTGTGAGAGAGGCTCTTTC 357

QY 301 GTGTACAAAGTGAAGATCTCTGGGCAACAACTTCCCGGCGACGGGCCCGTGTATGACGAAC 360

Db 358 ATCTCAAGAGTGAAGTTCAATCGGCGGTGAATCTCCCTCCGAGGGGCCCGTAATAGCAGAAAG 417

QY 361 AAGGGCGGCGCGCTGTGGAGGCGCTTCACCCGAGATCTGTATAGAGGTGAACGGCGTCTGGCGC 420

Db 418 AAGACCAATGGGCTGTGGAGGCGCTTCACCTGAGCGCTGTATACCCCGGCGACGGCGTGTCAAG 477

QY 421 GGCCAGTCCAGCATGGCCCTGTGAGTGCCTCCGGCGGTGTGGCACCTGACTGACCTGCAC 480

Db 478 GGCGAGATTCACAAAGGCCCTTGAAGCTGAAGGACGGCGGCACATCACTGTGGAGTTCAAG 537

QY 481 ACCACTTACCGGTCCCAAGAAAGCCCGCTCTCGGCTTGAAGATGTCCGGCTTTCACCTTCGAG 540

Db 538 AGTACTTACATGGGCCCAAGAAAGCCG-----TGCACCTGCCCGGCTTACTACATACGAG 588

QY 541 GACCAACCCCATCGAGATCTGTGAGGAGGTGAGAAAGGGAAGTGTCAACAGCAGTACGAG 600

Db 589 GACTCCAAAGCTGGACATCACTCCCAACAAGAGACTACACATCTGTGAGAGCAGTACGAG 648

QY 601 GCCGCCGTGGGCGCGCTAC 618

Db 649 CGCACCGAGGCGCGGCAC 666

```

RESULT 2
US-09-839-650-1
; Sequence 1, Application US/09839650
; Patent No. 6645761
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
; Patent No. 6645761
; TITLE OF INVENTION: Fluorescent Protein
; FILE REFERENCE: 25436/1755
; CURRENT APPLICATION NUMBER: US/09/839,650
; CURRENT FILING DATE: 2001-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Humanized R. mulleri polynucleotide
; NAME/KEY: misc_feature
; LOCATION: (1)..(720)
; OTHER INFORMATION: Humanized DNA sequence
US-09-839-650-1

```

Query Match	34.3%;	Score 224.6;	DB 4;	Length 720;
Best Local Similarity	62.8%;	Pred. No. 4,5e-38;		
Matches 385; Conservative	0;	Mismatches 219;	Indels 9;	Gaps 2

Qy	1	GAGGGCAACCGGAAAGGGCACTACTTCAAGTGCACCCGGAAAGGGGAAACCCCTC	60
Db	67	GAGGGCACTCGTGAACAAACCACTGTTCACATGAGAGGCTGCGGCAAGGGCAACATCCG	126
Qy	61	GAGGGCAACCCAGAGATGAAGATCGAGGTGATCGAGGGCGGCCCTTGCCCTTCGCTTC	120
Db	127	TTCCGCAACCAAGCTGTGTCAGATCCGCGTGAACAAAGGGCGCCCTTGCCCTTCGCTTC	186
Qy	121	CACATCTCTGCACCTCTCTGCATGTACGAGCTTCAAGGCTTCATCAAGTACGTGTCCGAC	180
Db	187	GACATCTGAGACCCCGCTTCCAGTACGAGCAACCGCACTTCAACAAATGCCCAACGAC	246
Qy	181	ATCCCCGACTACTTCAGCAAGTCCCTCCCGAGGGCTTCACTTGGAGAGGCAACCAAC	240
Db	247	ATTCAGCACTACTTCATCCAGAGCTTCCCGCGGCTTCATGTACGAGGGCAACCTTGGC	306

QY	241	TACGAGAGAGCGGCTTCTTACACCGGCCACAGAGAACTCCTCTGAGCGGCACCTGCTG	300
Db	307	TACGAGAGACGGGCGCTGTGTGAGATCCCGACGACATCAACTGATTCGAGGACAAAGTTT	366
QY	301	GTGTACAAGGTGAAGATCTGTGGCAACAACCTTCCCGCGGACGGGCCCGGTGATGCAGAAC	368
Db	367	GTGTACCGGCTGTGAGTACAAGGGACGACAACTTCTCCGACGACGGGCCCGGTGATGCAGAAC	426
QY	361	AAGGCGGCGCGCTGGGAGCGCTTCACCGAGATCGTGTACGAGGTGACGGCGTGTGCGC	420
Db	427	ACCATCTGGGCGATCGAGCCGACGCTTCGAGGCGCATGTACATGAACAACGGCGTGTGTTG	486
QY	421	GGCCAGTCCAGATATGCGCTGGAAGTGCCTCCGCGCGTGTGCGCACCTTACCTTGACCTTGAC	480
Db	487	GGCGAGGTGATCTGTGTGTACAAGCTGAAACAACGGCGAATCTACAGCTGCGCCACATGAAG	546
QY	481	ACCACCTACCGGCTCCAGAGAGCGCGCTCCGCGCTGAAATGCGCGGCTTCCACTTCGAG	540
Db	547	AC-----CTGTATAGAGCAAGGCGGTGTGAAGAAATTCCCTCTTACCACTTCATC	600
QY	541	GACCAACCGCATCGAGATCTGTGAGGAGGTGGAAGGGCAAGTGTACAAGCAGTACGAG	600
Db	601	CAGCAACCGCTGGAAGAAA--AGACTACGTGAGAGACGGCGGCTTGTGTGAGGACGACGAG	657
QY	601	GGCGGCGTGGGCGC	613
Db	658	ACCGCCATCGGCC	670

```

RESULT 3
US-09-977-897-1
; Sequence 1, Application US/09977897
; Patent No. 6780974
; GENERAL INFORMATION:
; APPLICANT: Chen, Yih-Tai
; APPLICANT: Cao, Longguang
; TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluoresce
; TITLE OF INVENTION: protein with codon preference of mammalian expression systems an
; FILE REFERENCE: 41856-5
; CURRENT APPLICATION NUMBER: US/09/977, 897
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
US-09-977-897-1

```

Query Match	34.1%	Score 223;	DB 4;	Length 1482;
Best Local Similarity	62.6%;	Pred. NO. 1.1e-37;		
Matches 384; Conservative	0;	Mismatches 220;	Indels 9;	Gaps 2;

QY 1 NAGGGGCAACGGGACCGGCACTACTTTCAGTAGTGACCCGGCAAGGGGGCAACCCCTTC 60

Db 79 GAGGGGCACTCGGAAACCAACCGCTTTCAGCATGAGGGGCTTCGGCAAGGGCAACGTCGTG 138

QY 61 GAGGGCAACCCAGAGAGATGAAGATCGAGGTGATCGAGGGCGGCCCCCTTCGCTTCGCTTC 120

Db 139 TTCCGGCAACCAAGCTGATGACATCCGGGGGACCAAGGGGGGCGCTTCGCTTCGCTTC 198

QY 121 CACATCCTGTGCACCTCCTGCATGTAGGGCTTCAGAGGCTTTCATCAAGTACGTGTCCGGC 180

Db 199 GACATCGGACATCGCTTCCTTCAGTACGGCAACCGAACCTTTCACCAAGTATCCGACGAC 258

QY 181 ATCCCGGACTTTCAGACAGTCCCTCCCGGAGGGCTTCACCTGGAGGGGCAACCAACC 240

Db 259 ATCCCGGACTTTCGTGTGACAGCTTCCCTGCGGCTTCTTTCAGAGGGGAACCTGGGG 318

QY 241 TACAGAGACGGCGGCTTCTCTAGCGGCCCAACAGACAACCTCCCTGGAGCGGCACTGCTTG 300

Db 319 TTCCAGAGACGGCGGCTTCTGTGACATTCGAGCGGCAATCAGCTCTGGAGGACCAACAAGTTC 378

```
QY 301 GTGTCAAGAGTGAAGATCTCTGGCAACAATTCCCGCCGAGCCCGCTGATGAGAAC 360
    |||
DB 379 CACTACAGAGTGAAGATCCCGGCAACAATTCCCGGCAACGCGCCCTGTATGAGAAC 438
    |||
QY 361 AAGGCGGCGCTGGAGAGCCCTTCACCGAGATCGTGTACAGAGTGAAGCGGCTGTGCGC 420
    |||
DB 439 GCGATCTGTGGCATGAGAGCCGACGCTTCGAGGTGTGTATCATGAACAAGCGGCTGTGCTG 498
    |||
QY 421 GCGGCGTCAAGATGAGCGCTGTGAGAGCCCGGCGGTGCGCACTGACCTGCACTGCGAC 480
    |||
DB 499 GCGGAGTGTGAGCTGTGTATCAAGCTGAGAGAGCGGCACTTACTACAGCTGCGCACTGAAG 558
    |||
QY 481 ACCACTTACCGCTCCAAAGAGCCCGCTCGCCCTGAAGATGCGCGGCTTCACCTTCGAG 540
    |||
DB 559 ACCCTTACCGGAGAGAG-----GCGGCGTGAAGAGATTCCTGTGATCACTTATTCATC 612
    |||
QY 541 GACCAACCGCATGAGATCTCTGAGAGAGTGAAGAGGCGCAAGTGTCAAGACAGTACGAG 600
    |||
DB 613 CACCAACCGGCTGAGAG---AGAACTACGTGAGAGAGGAGGAGCTTGTGTGAGCAGACGAG 669
    |||
QY 601 GCGGCGGTGGGCGC 613
    |||
DB 670 ACCGCGATGCGCC 682
    |||
```

RESULT 4

```
US-09-459-956-7
; Sequence 7, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, Iii, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Clavularia sp
US-09-459-956-7
```

Query Match 25.5%; Score 167; DB 3; Length 801;

Best Local Similarity 55.7%; Pred. No. 5e-26;

Matches 345; Conservative 0; Mismatches 265; Indels 9; Gaps 1;

```
QY 1 GAGGGCACCGTGAACGGCCACTACTTCAAGTGCACCGGCAAGGCGAGGCAACCCCTTC 60
    |||
DB 169 GAAGAAATGTAAACGGGATGCTTTTGTGATGAAGAGAAAGAAAGAAAGCCTTAC 228
    |||
QY 61 GAGGGCACCCAGAGATGAAGATCGAGTGAAGAGGCGGCGCCCTGCTTGCCTTC 120
    |||
DB 229 GATGGGACACACACTTTAACTCGAAGTGAAGAGAGGCGGCTGTGCTTTTCTTAC 288
    |||
QY 121 CACATCTCTGTCACTCTGTGATGTAAGGCTCCAGGCTTCATCAAGTACGTGCGGC 180
    |||
DB 289 GATATCTGTCAACCGCTTCCAGTACGGAACAGAGCATTTGCAAAATATCCAGACGAT 348
    |||
QY 181 ATCCCGACTACTTCAAGAGATCCCTCCCGAGAGGCTTCACTGGGAGGCAACCAAC 240
    |||
DB 349 ATAGCAACTATTTCAAGAGATGCTTCCGAGAGGATTTCTCGGAAAAAAGACATGACT 408
    |||
QY 241 TAGAGAGAGCGGCGCTTCTGTGACCGGCCACAGACACTCTCTGAGCGGCACTGCTG 300
    |||
```

```
DB 409 TTTGAAGCAAAAGCATTTGTCAAGTGAAGAAAGTGCATATAGCATGAGAGAACTCTTT 468
    |||
QY 301 GTGTCAAGAGTGAAGATCTCTGGCAACAATTCCCGGCAACGCGCCCGTATGAGAAC 360
    |||
DB 469 ATCTATGAATTTGTTTGTGATGAGATGAACCTTCTCCCAATGTCGCGTTATGAGAAA 528
    |||
QY 361 AAGGCGGCGCTGGAGAGCCCTTCACCGAGATCGTGTACAGAGTGAAGCGGCTGTGCGC 420
    |||
DB 529 AAAACTTTGAAGTGGAAACATCCTGAGATTAATGATGCGGTGATGAGATGCTGTGTC 588
    |||
QY 421 GCGGAGTCAGATGAGCGCTGTGAGAGTCCCGGCGGTGCGCACTGACCTGCACTGAC 480
    |||
DB 589 GGAAGATATTAGCATTTCTGTTGTGAGAGGAGGTGACCATTAACGATGTACTTCAAA 648
    |||
QY 481 ACCACTTACCGCTCCAAAGAGCCCGCTTCGCGCTGAAGATGCGCGGCTTCACCTTCGAG 540
    |||
DB 649 AGTATTTCAAAAGCAAAAAAGTTGTC-----AAATGCGAGACTATCACTTTGTG 699
    |||
QY 541 GACCAACCGCATGAGATCTCTGAGAGAGTGAAGAGGCAAGTGTCTAAGACAGTACGAG 600
    |||
DB 700 GACCATCGCATTTGAGATCTTGAACCATGACAAAGATTTACAAACAAAGTAACTGTATGAG 759
    |||
QY 601 GCGGCGGTGGGCGGCTACT 619
    |||
DB 760 AATGCAAGTTGCTCGCTATT 778
    |||
```

RESULT 5

```
US-09-459-956-5
; Sequence 5, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, Iii, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Discosoma striata
US-09-459-956-5
```

Query Match 23.4%; Score 152.8; DB 3; Length 699;

Best Local Similarity 54.2%; Pred. No. 4.5e-23;

Matches 335; Conservative 0; Mismatches 277; Indels 6; Gaps 1;

```
QY 1 GAGGGCACCGTGAACGGCCACTACTTCAAGTGCACCGGCAAGGCGAGGCAACCCCTTC 60
    |||
DB 55 GAAGAAAGCTTCAAGAGGACACTACTTGAATTAAGCAAGAAAGAAAGAGACGCTTAT 114
    |||
QY 61 GAGGGCACCCAGAGATGAAGATCGAGTGAAGAGGCGGCGCCCTGCTTGCCTTC 120
    |||
DB 115 GAAGGACCAATATCCGTCACTGAGGTACCAAGGTTGACAGCTGTGCAATTTGTTGG 174
    |||
QY 121 CACATCTCTGTCACTCTGTGATGTAAGGCTCCAGGCTTCATCAAGTACGTGCGGC 180
    |||
DB 175 CATATTTTGTGCCAATTTTCAATATGAGAAAGAGCATTTGTCCACACCTGACAAAC 234
    |||
QY 181 ATCCCGACTACTTCAAGAGATCCCTCCCGAGAGGCTTCACTGGGAGGCAACCAAC 240
    |||
DB 235 ATACATGATATTTCTAAAGCTGTCAATTTCCGAGGAGTATTAATGGAAGAGGTCAATGAC 294
    |||
```

	Query Match	Similarity	23.1%	Score 151.4	DB 3	length 678
	Best Local	Similarity	56.2%	Pred. No. 8.8e-23		
	Matches	284	Conservative	0	Mismatches 221	Indels 0; Gaps 0
QY	1	GAGGGACCGTGAAACGGCCACTTCAAGTGCACCGGCAAGGGCGAGG3CAACCCCTTC	60			
Db	55	GAAAGAAACGGTCAATGGGCACAGATTGAAATAGAAGCGAAGAGAGAGGGGACATAC	114			
QY	61	GAGGGACCCACGAGATGATGATCGAGTGCAGTGCAGGGCGGGCCCTGGCCCTCGGCTTC	120			
Db	115	GAAGGCCACAATACCGTAAAGCTTAAAGTAAACCAAGGGGGACCTTTGCCATTGTGTTGG	174			
QY	121	CACATCTGTGCCACTCTCGCATGTACGGCTCCAAAGGSCCTTATCAATGATGCTGTCCGGC	180			
Db	175	GATATTTTGTACCAACAATTTCAATATGGAAGCAAGTATATGTCAAGACACCCCTGGAC	234			
QY	181	ATCCCGCACTACTTCAGCAGTCCCTCCCGGAGGGCTTACCTGGAGGCGCACACACACC	240			

Query Match	18.8%	Score 122.8	DB 3	Length 690
Best Local Similarity	52.6%	Pred. No. 8.4e-17		
Matches	324	Conservative	0	Mismatches 277, Indels 15, Gaps 2
QY	1	GAGGGCACCGTGAAAGGCGGCACCTACTCTCAAGTACACCGGCAAGGGCGAAGGGCAACCCCTTC	60	
DB	55	GATGGCTGTGTCATATGGGCATTACTTTACCTTCAAGGTAAGGCAACGGGAAGGCATAC	114	
QY	61	GAGGGCACCCA-----GAGATGAAGAATCGAGGATGTAAGAGGGGGGGCCCTCGCCCTTC	114	
DB	115	GAAAGGAGCGACGACTTCGACTTTTAAAGTACACATGAGCCAGCGTGGGCCCTTGGCATTC	174	
QY	115	GCCTTCCACATCTCTGTCCACCTCTCGATGTACGGCTCCAAAGCCCTTCATCAAGTACGTG	174	
DB	175	TCCTTTGACATTCATCTACAGTGTTCAAATATGAAATATGCATGTCTTTCTGCGTATCT	234	
QY	175	TCCGGCATCCCGGACTACTCTCAAGAGAGTCCCGCCGAGGGCTTCAACCGAGGGCGCAC	234	
DB	235	ACCGTATGCCCGACTATTTTCAACAAGCATTTTCTGACGGAATGTCATATGAAGAAGCT	294	
QY	235	ACCACTTACAGAGACGAGCGGCTTCTCTGACCGGCCACCAAGACACCTTCCCTGACGCGAC	294	
DB	295	TTTACCTTATGAAGATGAGAGAGTTCTCTACAGCAGTGGGAATATAGCCTTTAAGGCAAC	354	


```
QY 295 TGCCCTGTGTAGAGTGAAGTCTCTGGGCAACACTTCCCGCGGAGCGCCCGGTGATG 354
|||
DB 355 TCGTTTGAGACAAATTCACGTTTCATGAGTGAAGTCTTCTGCTGATGACCTGTGATG 414
|||
QY 355 CAGAACAGAGCGCGCGCTGGAGAGCCCTTCCACCGAGATGCTGTACAGATGAGCGCGTG 414
|||
DB 415 GCGAAGAGAGCAACTGTGTTGGAGACCCATTTTGGAGAAAATGACTGTCTGCGATGAAAT 474
|||
QY 415 CTGCGCGGCGAGTCCAGATGAGCGCCCTGGAGTGCCTCCGCGGTGCGCACTGACTGCGAC 474
|||
DB 475 TTGAAGGGGTGATGTCAACCGCGTTTCTCATGTGCAAGGAGTGGCAATTACAGATGCCAA 534
|||
QY 475 CTGCAACACCACTTACCGCTTCCAAAGAGCCCGCTCCGCGCTGAAGATGCGCGGCTTCCAC 534
|||
DB 535 TTCCACACTTCTTACAAAGCAAAAACCGG-----TGAAGATGCCAACAAACAT 585
|||
QY 535 TTCCAGAGACCAACCGCATCGAGATCTCTGAGAGAGTGAAGAGGCAAGGCTTACAGAG 594
|||
DB 586 GTGTGTGAACATGCTGCTTTCGAGAGACCGACCTTGAACAAAGTGGCAAGTGTTCAGCTG 645
|||
QY 595 TACGAGCGCGCGCTGG 610
|||
DB 646 ACGAGACAGCTGTG 661
|||
```

RESULT 8

```
US-09-486-241-31
; Sequence 31, Application US/09486241
; Patent No. 6472184
; GENERAL INFORMATION:
; APPLICANT: Hegemann, Peter
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEIC ACID
; FILE REFERENCE: 3910/06706
; CURRENT APPLICATION NUMBER: US/09/486,241
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/05219
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: DE19736591.4
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified gene from Agurea victorea
US-09-486-241-31
```

```
Query Match 16.9%; Score 110.6; DB 4; Length 717;
Best Local Similarity 52.5%; Pred. No. 3e-14;
Matches 342; Conservative 0; Mismatches 294; Indels 15; Gaps 4;
```

```
QY 1 GAGGGACCGGTGAACGGCCACTTCTTCAAGTGAACGGGAGGCGAGGCAACCCCGTC 60
|||
DB 55 GACGGGAGAGTGAACGGCCCAAGTTCCTCGTTCGGGAGGAGTGAAGGTCGCGCAC 114
|||
QY 61 GAGGGACCGAGAGATGAAGATCGAGTGAATGAGGAGGCGCGCCCTGCGCTTCCGCTTC 120
|||
DB 115 TACGGCAAGTGAACCTTGAAGTTCATCTGCAACAC---CGGCAAGTTCGCGCGCTG 171
|||
QY 121 CACATCTGTCCACTCTGATGATAGCGGTCCAGAGGCTTCATCAAGTGTGTCGGC 180
|||
DB 172 CCGACCTGGTCAACACTTCACTACGAGTGTCAAGTGTCTTCCGCTACCCGACAC 231
|||
QY 181 AT-----CCCGACACTTCAAGAGAGTCCCTCCCGAGGAGGCTTCACTCGGAGGCGAC 234
|||
DB 232 ATGAAGACAGACGACTTCTTCAAGTCCGATCCGAGGAGTGAAGTGAAGGAGGAGC 291
|||
QY 235 ACCACCTAGAGAGAGCGGCGCTTCTGACCGCCACAGAGACCTTCCCTGAGCGGAG 294
|||
DB 292 ATCTTCTTCAAGAGACGAGCAACTCAAGACCCGCGCGAGGTCAAGTTGAGGGCGAG 351
|||
```

```
QY 295 TGCCCTGTGTAGAGTGAAGTCTCTGGGCAACAACTTCCCGCGGAGCGCCCGGTGATG 354
|||
DB 352 ACCCTGTGAACCGCATGAGCTGAAGGCAATCGACTTCAAGAGAGAGGCAACACTTCTG 411
|||
QY 355 CAGAACAGAGCGCGCGCTGGAGAGCCCTTCCACCGAGATGCTGTACAGATGAGCGCGTG 414
|||
DB 412 GCGCAAGAGCTG---AATTACACTCAAACTTCCCAAGAGTGTATCATATGCGCGACAG 468
|||
QY 415 CTGCGCGGCGAGTCCAGATGAGCGCCCTGGAGTGCCTCCGCGGTGCGCACTGACTGCGAC 474
|||
DB 469 CAGAAAGACGCGATCAAGTGAAGTCAAGATCC---GCAACATCGAGGACGCGTCC 525
|||
QY 475 CTGCAACACCACTTACCGCTTCCAAAGAGCCCGCTCCGCGCTGAAGATGCGCGGCTTCCAC 534
|||
DB 526 GTGCACTGCGCGACACTTACCGAGAAACCCCATCGGAGATGCGCCGCTGCTG 585
|||
QY 535 TTCCAGAGACCAACCGCATCGAGTCTCTGAGAGAGTGAAGAGGCAAGTGTACAGAG 594
|||
DB 586 CCGACAAACCACTACTGTCCACCGATCCGCGCTGTCCAGAGACCCCAAGAGAGAGCGC 645
|||
QY 595 TACGAGCGCGCGCTGGCGCTACTGCGACGCGCGCCCTCCAGCTGGC 645
|||
DB 646 GACCATATGTCTCTGAGAGTTCGTCAACCGCTGCGCGATCACCGAGC 696
|||
```

RESULT 9

```
US-08-532-390-40
; Sequence 40, Application US/08532390
; Patent No. 5795737
; GENERAL INFORMATION:
; APPLICANT: SEED, BRIAN
; TITLE OF INVENTION: High Level Expression of Proteins
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,390
; FILING DATE: 22-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/324,243
; FILING DATE: 19-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LECH, KAREN F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/294001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-532-390-40
```

```
Query Match 16.2%; Score 105.8; DB 1; Length 762;
Best Local Similarity 52.1%; Pred. No. 3e-13;
Matches 339; Conservative 0; Mismatches 297; Indels 15; Gaps 4;
```

```

QY      1 GAGGCAACCGTGAACGGCCACTACTTCAAGTGCAACCGGCAAGGGGCAACCCCTTC 60
DB      85 GACGGCGACGTGAACGGCCCAAGTTTCAAGCTGTCCGGGAGAGGGCGAATGGCACCC 144
QY      61 GAGGGCAACCGGAGATGAAGATCGAGGTGATCGAGGGGCGCCCTGCTTCCCTTC 120
DB      145 TACGGCAAGCTGACCCCTGAAGTTCAATCTGCAACAC--CGGCAAGCTGCGCTGCTGG 201
QY      121 CACATCTGTGCACTCTCTGCAATGTAACGCTCCAAAGGCTTATCAAGTGTGCTGG 180
DB      202 CCCACCTGTGACCACTTCAAGCTCAACGCGTGAAGTGTTCAGCCGCTAACCCGACAC 261
QY      181 AT-----CCCCGACTACTTCAAGCAAGTCCCTCCCGAGGGGCTTCACTCGGAGCGCAC 234
DB      262 ATGAAGCAAGCAAGCTTCTTCAAGTCCGCAATGCTCCGAGGCTTACGACGAGCGCAC 321
QY      235 ACCACCTTACGAGCAAGCGCGCTTCTGACCGGCCCAACAGACACTCCCTGAGCGGAC 294
DB      322 ATCTTCTTCAAGGACGACGGCAACTCAAGAACCCCGCGGAGGTGAAGTTGAGGGCGAC 381
QY      295 TGCCGTGTGTAACAAGTGAAGTCTTGGGCAACAATTCCTCCCGGAGCGGCTGATG 354
DB      382 ACCCTGTGAACCGCATGCAAGTGAAGGGCATGCACTTCAAGAGAGACGGCAACATCTG 441
QY      355 CAGAACAGAGCGCGCGCTGGAGCCCTTCAACGAGATGTGTGACAGGTGAGCGCGTG 414
DB      442 GGGCAAGCTGG---AGTAACTAACAACAGACCAACAGCTTATATATATGCGCACAG 498
QY      415 CTGCGCGGCGCATGCGAGATGCGCTGAGAGTCCCGCGCGGTGCGCACCTGACCTGCAC 474
DB      499 CAGAAAGACGGCATCAAGGTGAATTTCAAGATCC--GCCAACATGAGAGACGGCAGC 555
QY      445 CTGACACACCACTACCGCTCCCAAGAACGCCGCTCCGCTGGAAGATGCGGCTTCCAC 534
DB      556 GTGACGCTGCGGACCACTACCAAGCAACACCCCATGCGGAGGCGCGCTGTGCTG 615
QY      535 TTGCGAGCAACCGGATGAGATCTTGGAGAGGTGAGAGAGGCAAGTGTCAACAGAG 594
DB      616 CCCGCAACCACTAATCTGAGACCCCAATGCGGCTGAGACCAAGACCCCAACGAGAGCG 675
QY      595 TACGAGCGCGCGTGGCGCGCTACTGCGACCGCGCGCCCTCCAGCTGCGC 645
DB      676 GATCACAATGTCTGTGGAAGTTGCTGACCGCGCGGAGATCACTACGCGC 726

RESULT 10
US-08-717-294-40
; Sequence 40, Application US/08717294
; Patent No. 6114148
; GENERAL INFORMATION:
; APPLICANT: SEED, BRIAN
; APPLICANT: HAAS, JURGEN
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Ribling LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,294
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Eibling, Karen L.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/345001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
;
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 762 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: Other
;
; US-08-717-294-40

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Query Match      16.2%; Score 105.8; DB 3; Length 762;
Best Local Similarity 52.1%; Pred. No. 3e-13;
Matches 339; Conservative 0; Mismatches 297; Indels 15; Gaps 4;

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QY      1 GAGGCAACCGTGAACGGCCACTACTTCAAGTGCAACCGGCAAGGGGCAACCCCTTC 60
DB      85 GACGGCGACGTGAACGGCCCAAGTTTCAAGCTGTCCGGGAGAGGGCGAATGGCACCC 144
QY      61 GAGGGCAACCGGAGATGAAGATCGAGGTGATCGAGGGGCGCCCTGCTTCCCTTC 120
DB      145 TACGGCAAGCTGACCCCTGAAGTTCAATCTGCAACAC--CGGCAAGCTGCGCTGCTGG 201
QY      121 CACATCTGTGCACTCTCTGCAATGTAACGCTCCAAAGGCTTATCAAGTGTGCTGG 180
DB      202 CCCACCTGTGACCACTTCAAGCTCAACGCGTGAAGTGTTCAGCCGCTAACCCGACAC 261
QY      181 AT-----CCCCGACTACTTCAAGCAAGTCCCTCCCGAGGGGCTTCACTCGGAGCGCAC 234
DB      262 ATGAAGCAAGCAAGCTTCTTCAAGTCCGCAATGCTCCGAGGCTTATGTCAGAGACGCAAC 321
QY      235 ACCACCTTACGAGCAAGCGCGCTTCTGAGAGTCCCGGCCCAACAGACACTCCCTGAGCGGAC 294
DB      322 ATCTTCTTCAAGGACGACGGCAACTCAAGAACCCCGCGGAGGTGAAGTTGAGGGCGAC 381
QY      295 TGCCGTGTGTAACAAGTGAAGATCTTGGGCAACAATTCCTCCCGGAGCGGCTGATG 354
DB      382 ACCCTGTGAACCGCATGCAAGTGAAGGGCATGCACTTCAAGAGAGACGGCAACATCTG 441
QY      355 CAGAACAGAGCGCGCGCTGGAGCCCTTCAACGAGATGTGTGACAGGTGAGCGCGTG 414
DB      442 GGGCAAGCTGG---AGTAACTAACAACAGACCAACAGCTTATATATGCGCACAG 498
QY      415 CTGCGCGGCGCATGCGAGATGCGCTGAGAGTCCCGCGCGGTGCGCACCTGACCTGCAC 474
DB      499 CAGAAAGACGGCATCAAGGTGAATTTCAAGATCC--GCCAACATGAGAGACGGCAGC 555
QY      445 CTGACACACCACTACCGCTCCCAAGAACGCCGCTCCGCTGGAAGATGCGGCTTCCAC 534
DB      556 GTGACGCTGCGGACCACTAATCTGAGACCCCAATGCGGCTGAGACCAAGACCCCAACGAGAGCG 615
QY      535 TTGCGAGCAACCGGATGAGATCTTGGAGAGGTGAGAGAGGCAAGTGTCAACAGAG 594
DB      616 CCCGCAACCACTAATCTGAGACCCCAATGCGGCTGAGACCAAGACCCCAACGAGAGCG 675
QY      595 TACGAGCGCGCGTGGCGCGCTACTGCGACCGCGCGCCCTCCAGCTGCGC 645
DB      676 GATCACAATGTCTGTGGAAGTTGCTGACCGCGCGGAGATCACTACGCGC 726

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RESULT 11
US-09-277-716-30
; Sequence 30, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:

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; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; FILE REFERENCE: 24729-121B
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptiliosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; FEATURE:
; OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (Insert A)
US-09-277-716-30
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Query Match      16.1%; Score 105; DB 3; Length 1104;
Best Local Similarity 50.7%; Pred. No. 4,8e-13;
Matches 252; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
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QY      1 GAGGCGACCGGTGAAGCGGCACCTACTTCAAGTGCACCGGAGGCGGAGGCGAACCCTTC 60
DB      97 GAGGAAATCGTGAACAATACGTTTTTTCATGAGAGATTGGAAAGGCAATGTATTA 156
QY      61 GAGGCGACCGGAGAGATGAAGATCGAGTGCAGGCGGCGCCCTTCGCTTC 120
DB      157 TTTGGAACAATGATGCAATCGGGTTACAAAGGAGGTCCTGTCATTGCTTTC 216
QY      121 CACATCTGTCACCTCTGCGATGACGCTCCAAAGGCTTCATCAAGTGTGTCGGC 180
DB      217 GATATTTGTTCCATAGCTTTCCAAATACGGGAATCGCATTTTCAGAAATACCAAGAC 276
QY      181 ATCCCGACTACTTCAAGCAGTCCCTCCCGAGGGCTTCACTGGAGGCGACACACC 240
DB      277 ATTGGGACTACTTTGTTCAATCATTTCCGCGTGATTTTCTAGAAAGAAATCTAGCC 336
QY      241 TACGAGACGGGCGCTTCTGACCGGCCACAGACACCTCCCTGACGCGACTGCTG 300
DB      337 TTTGGAAGATGGCGCATTTGTGACATTCGTTCAATATAGTTTAGAAGATGATTAATTC 396
QY      301 GTGTCAAGGTGAAGATCTGTGGCAACAATTCCTCCGCGAGCGGCTGTATGCAAGC 360
DB      397 CACTCAAAAGTGAATATAGAGCAACGGTTTCCCTAGTAAAGCAACCCGTATGCAAAA 456
QY      361 AAGGCGGCGCGTGGAGGCGCTTCCACCGAGATCGTGTACAGGTGAGCGGCGTGGCGC 420
DB      457 GCCATCTCTGGATGAGGCAATCTTTGAGGTGTCTATACATAAGCGGCGTTTCTGGTG 516
QY      421 GGCAGTCACAGATGCGCTTGGAGCGCCCGCGGCTGCGCACCTGACCTGCGAC 480
DB      517 GCGGAAGTATCTGTTTACAAACTCGAGTCAAGGAACTATTACTCGTGCCACATGAAA 576
QY      481 ACCACTACCGCTCCAA 497
DB      577 ACGTTTACAGATCCAA 593
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RESULT 12
US-09-609-161B-30
; Sequence 30, Application US/09609161B
; Patent No. 643682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
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; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LU
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HT
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptiliosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; OTHER INFORMATION: Ptiliosarcus Green Fluorescent Protein (GFP) (Insert A)
US-09-609-161B-30
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Query Match      16.1%; Score 105; DB 3; Length 1104;
Best Local Similarity 50.7%; Pred. No. 4,8e-13;
Matches 252; Conservative 0; Mismatches 245; Indels 0; Gaps 0;
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QY      1 GAGGCGACCGGTGAAGCGGCACCTACTTCAAGTGCACCGGAGGCGGAGGCGAACCCTTC 60
DB      97 GAGGAAATCGTGAACAATACGTTTTTTCATGAGAGATTGGAAAGGCAATGTATTA 156
QY      61 GAGGCGACCGGAGAGATGAAGATCGAGTGCAGGCGGCGCCCTTCGCTTC 120
DB      157 TTTGGAACAATGATGCAATCGGGTTACAAAGGAGGTCCTGTCATTGCTTTC 216
QY      121 CACATCTGTCACCTCTGCGATGACGCTCCAAAGGCTTCATCAAGTGTGTCGGC 180
DB      217 GATATTTGTTCCATAGCTTTCCAAATACGGGAATCGCATTTTCAGAAATACCAAGAC 276
QY      181 ATCCCGACTACTTCAAGCAGTCCCTCCCGAGGGCTTCACTGGAGGCGACACACC 240
DB      277 ATTGGGACTACTTTGTTCAATCATTTCCGCGTGATTTTCTAGAAAGAAATCTAGCC 336
QY      241 TACGAGACGGGCGCTTCTGACCGGCCACAGACACCTCCCTGACGCGACTGCTG 300
DB      337 TTTGGAAGATGGCGCATTTGTGACATTCGTTCAATATAGTTTAGAAGATGATTAATTC 396
QY      301 GTGTCAAGGTGAAGATCTGTGGCAACAATTCCTCCGCGAGCGGCTGTATGCAAGC 360
DB      397 CACTCAAAAGTGAATATAGAGCAACGGTTTCCCTAGTAAAGCAACCCGTATGCAAAA 456
QY      361 AAGGCGGCGCGTGGAGGCGCTTCCACCGAGATCGTGTACAGGTGAGCGGCGTGGCGC 420
DB      457 GCCATCTCTGGATGAGGCAATCTTTGAGGTGTCTATACATAAGCGGCGTTTCTGGTG 516
QY      421 GGCAGTCACAGATGCGCTTGGAGCGCCCGCGGCTGCGCACCTGACCTGCGACCTGCGAC 480
DB      517 GCGGAAGTATCTGTTTACAAACTCGAGTCAAGGAACTATTACTCGTGCCACATGAAA 576
QY      481 ACCACTACCGCTCCAA 497
DB      577 ACGTTTACAGATCCAA 593
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RESULT 13
US-09-277-716-31
; Sequence 31, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
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1  APPLICANT: PROLUME, LTD.
2  TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS ENCODING THE LUC
3  TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
4  TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
5  FILE REFERENCE: 24729-121B
6  CURRENT APPLICATION NUMBER: US/09/609,161B
7  CURRENT FILING DATE: 2000-06-30
8  PRIOR APPLICATION NUMBER: 09/277,716
9  PRIOR FILING DATE: 1999-03-26
10 PRIOR APPLICATION NUMBER: 60/102,939
11 PRIOR FILING DATE: 1998-10-01
12 PRIOR APPLICATION NUMBER: 60/089,367
13 PRIOR FILING DATE: 1998-06-15
14 PRIOR APPLICATION NUMBER: 60/079,624
15 PRIOR FILING DATE: 1998-03-27
16 NUMBER OF SEQ ID NOS: 32
17 SOFTWARE: PatentIn Ver. 2.0
18 SEQ ID NO 31
19 LENGTH: 1279
20 TYPE: DNA
21 ORGANISM: Ptilosarcus gurneyi
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: (7) .. (720)

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Query Match 16.1%; Score 105; DB 3; Length 1279;

	Matches	252;	Conservative	0;	Mismatches	245;	Indels	0;	Gaps	0;
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QY	61	GAGGGCACCGAGAGATGAAGATCGAAGTGCAGGGCGGCGCCCTCGCCTTC	120							
Db	130	TTTGGAAACCAATTGATGCAAAATCCGGGTTTCAAAAGGAAGTCCGTTGCCATTGCTTTC	189							
QY	121	CACATCTGTCCACTTCCTGCATGACGGCTCCAGGCTTCATCAAGTACGTGTCGGC	180							
Db	190	GACATTTGTTTCCATAGCTTTTCCAAATACGGGAATGCACTTTCAGAAATATCCAGACAC	249							
QY	181	ATCCCGCACTACTTCAAGCAAGTCCCTCCCGGAGGCTTCACTGGGAGCGACCAACAC	240							
Db	250	ATTGCGGACTACTTGTTCATATCAATTCCTCGCTGATTTTCTAGAAAGAAATATACG	309							
QY	241	TACGAGGACGGCGGCTTCTGCAGCCGCCACAGGACCTTCCTGAGCGGCGACTGCTG	300							
Db	310	TTTGAAATATGGCGCATGTTGTGACATTCGTTCAAGATTAAGTTTAGAAGATGATGATTTC	369							
QY	301	GTGTACAAAGGTGAAGATCTGGGCAACAATCCCGGCGGACGGCGCCGTATCAGAAC	360							
Db	370	CACTCAAAAGTGAAGTATAGAGGCAACGGTTTCCCTTAGTACGGAACCCGTATGCAAAA	429							
QY	361	AAGCGCGGCGCTGGAGAGCCCTCCACCGAGATCGTGTAGAGGTGAACGGGCTGCGC	420							
Db	430	GCCATCTCGGCGATGAGCCATCGTTGAGGTGGTCAATGAACAACGGGCGTCTGGTG	489							
QY	421	GGCGAGTGCAGANTGGCCCTGGAAGTGCCTCGGCGGTGGCACTGCAGCTGCACTGCAC	480							
Db	490	GGGGAAGTATGCTCGTTTACAAATCGAGTCAAGGGAACATTTACTGTCGCCACATGAA	549							
QY	481	ACCACTTACGCTTCCAA	497							

RESULT 15
US-09-811-361-2
; Sequence 2, Application US/09811361
; Patent No. 6730821
; GENERAL INFORMATION:

APPLICANT: Guenther, Catherine
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
TITLE OF INVENTION: RETINA-SPECIFIC NUCLEAR RECEPTOR GENE DISRUPTIONS
FILE REFERENCE: R-125
CURRENT APPLICATION NUMBER: US/09/811,361
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,348
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 6355
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Phage Vector
US-09-811-361-2

Query Match 15.9%; Score 104.2; DB 4; Length 6355;

Best Local Similarity 51.9%; Pred.No. 9.7e-13; Mismatches 298; Indels 15; Gaps 4;

Matches 338; Conservative 0; Mismatches 298; Indels 15; Gaps 4;

QY 1 GAGGGCACCCTGTAACGGCCACTACTTCAAGTGCACCGCAAGGGCGAAGCCCTTC 60
DB 666 GACGGCGACGTAAACGGCCCAAGATTCAAGCTGTCGGCGAGGGCGAGTGCACAC 725
QY 61 GAGGGCACCCTGTAACGGGTGATGAGGGCGGCGCCCTTCGCTTC 120
DB 726 TACGGCAAGTACCTGAAATTCATCTGCACAC---CGGCAGCTGCCCGCTCTGG 782
QY 121 CACATCCGTCCACTCTGCAATGAGGCTTCAAGGCTTCATCAAGTACGTCCGGC 180
DB 783 CCGACCTGTGACACCTGACCTGACCTGACGCTGACGCTTCAAGCTTCAAGCTGAC 842
QY 181 ATC-----CCGACTACTTCAAGAGTCCCTCCCGAGGGCTTCACTGAGGCGCAC 234
DB 843 ATGAAGCAGCAAGATTCTTCAAGTCCGCAATGCCGAAGGCTACGTCAAGAGGCGCAC 902
QY 235 ACCACTTACGAGAGCGGCGCTTCTGACCGCCCAACAGACACTCCCTGAGCGGCA 294
DB 903 ATCTTCTTCAAGGAGCAGCGCAATCAAGACCCCGCGAGTGAAGTTCAGAGGCGAC 962
QY 295 TGGCTGTGTACAGAGTGAAGTCTGAGGCAACACTTCCCGCGAGCGGCGGTGATG 354
DB 963 ACCCTGTGAACCGCATGAGCTGAAGGCGCATGACTTCAAGAGAGAGCGCAACATCTG 1022
QY 355 CAGAACAAAGCCCGCGCTGAGAGCCCTTCAACGAGATCGTGTACGAGGTGAGCGCGTG 414
DB 1023 GGGCAGACAGCTGG---AGTACAACTAACAGGCCACAAAGTCTATATCATGCGCAG 1079
QY 415 CTGCGCGGCGCAGTCAGATGAGCGCTTGAAGTGCCTCGGCGGTGCGCACCTGAC 474
DB 1080 CAGAACAAAGCGCATCAAGTGAATTCAGAAATCC---GCCACAAATCAGAGACCGGCA 1136
QY 475 CTGCAACACCTTACCGCTCCAAAGAGCCCGCTCGGCTGAGATGCCGCGCTTCCAC 534
DB 1137 GTGACGCTGCGACCATCTACAGCAACACCCCATGCGGAGCGCGCGTGTCTG 1196
QY 535 TTGAGAGCAACCGCATCGAGTCTTGAAGAGGTGAGAAAGGCAAGTGTACAGAGCAG 594
DB 1197 CCGGCAACCACTACTAGAGACCGAGTCCGCGCTGAGGAAAGACCCCAAGAGAGAGCGC 1256
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	654	100.0	654	US-10-081-864-23	Sequence 23, Appl
2	652.4	99.8	1404	US-10-806-930-7	Sequence 7, Appl
3	649.2	99.3	707	US-10-006-922-39	Sequence 39, Appl
4	649.2	99.3	707	US-10-081-864-21	Sequence 21, Appl
5	647.6	99.0	1398	US-10-806-930-9	Sequence 9, Appl
6	641.2	98.0	699	US-10-006-922-41	Sequence 41, Appl
7	623.8	95.4	686	US-10-724-178-17	Sequence 17, Appl
8	566.6	84.6	591	US-10-724-178-1046	Sequence 1046, Ap
9	487.4	74.5	555	US-10-724-178-1064	Sequence 1064, Ap
10	436.4	66.7	504	US-10-724-178-1060	Sequence 1060, Ap
11	415.8	63.6	696	US-10-006-922-13	Sequence 13, Appl

12	415.8	63.6	696	14	US-10-081-864-9	Sequence 9, Appl
13	412.4	63.1	767	14	US-10-155-809-1	Sequence 1, Appl
14	410.8	62.8	767	14	US-10-155-809-3	Sequence 3, Appl
15	409.2	62.6	767	14	US-10-155-809-5	Sequence 5, Appl
16	398	60.9	456	18	US-10-724-178-1052	Sequence 1052, Ap
17	396.8	60.7	687	9	US-09-976-673-13	Sequence 11, Appl
18	395.2	60.4	687	9	US-09-976-673-13	Sequence 13, Appl
19	395.2	60.4	1396	9	US-09-976-673-15	Sequence 15, Appl
20	395.2	60.4	1396	18	US-10-806-930-1	Sequence 1, Appl
21	395.2	60.4	1424	9	US-09-976-673-17	Sequence 17, Appl
22	395.2	60.4	1424	18	US-10-806-930-3	Sequence 3, Appl
23	382.8	58.5	405	18	US-10-724-178-1050	Sequence 1050, Ap
24	340.8	52.1	363	18	US-10-724-178-1058	Sequence 1058, Ap
25	300.4	45.9	681	14	US-10-121-258-7	Sequence 7, Appl
26	299.6	45.8	675	18	US-10-724-178-15	Sequence 15, Appl
27	299.6	45.8	678	14	US-10-121-258-9	Sequence 9, Appl
28	298.8	45.7	675	13	US-10-006-922-38	Sequence 38, Appl
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33	298.8	45.7	1050	13	US-10-060-857-7	Sequence 12, Appl
34	298.6	45.7	649	18	US-10-439-262-12	Sequence 36, Appl
35	297.2	45.4	678	13	US-10-006-922-36	Sequence 14, Appl
36	297.2	45.4	678	14	US-10-081-864-14	Sequence 5, Appl
37	297.2	45.4	678	16	US-10-121-258-5	Sequence 5, Appl
38	297.2	45.4	678	16	US-10-315-920-3	Sequence 5, Appl
39	297.2	45.4	678	16	US-10-315-920-5	Sequence 5, Appl
40	297.2	45.4	681	14	US-10-121-258-3	Sequence 3, Appl
41	297.2	45.4	681	14	US-10-121-258-23	Sequence 23, Appl
42	297.2	45.4	1638	15	US-10-214-932-51	Sequence 51, Appl
43	297.2	45.4	1647	15	US-10-214-932-75	Sequence 75, Appl
44	297.2	45.4	4692	15	US-10-161-403-29	Sequence 29, Appl
45	297.2	45.4	4692	18	US-10-435-640-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-10-081-864-23
; Sequence 23, Application US/10081864
; Publication No. US2003002287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yanushevich, Yurly
; APPLICANT: Savitsky, Alexandr
; APPLICANT: Pradkov, Arcady
; TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-23

Query Match 100.0%; Score 654; DB 14; Length 654;
Best Local Similarity 100.0%; Pred. No. 4.6e-154;
Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGACCGTGAAGGCGCCTACTTCAAGTGCACCGGCAAGGCGGCAACCCCTTC 60

Db 1 GAGGGCACCCGTGAACGGGCACTTACAGTGCACCGGCAGAGGCCAGGGCCAAACCCCTC 60

QY 61 GAGGGCACCCAGAGATGAAGATCGAGTGATCGAGGGCGGCCCCCTGACCCTTCGCTTC 120

Db 61 GAGGGCACCCAGAGATGAAGATCGAGTGATCGAGGGCGGCCCCCTGACCCTTCGCTTC 120

QY 121 CACATCTCTGCCACCTCTGCAGATGTAACGGTCCAGAGGCCCTTCAATCAAGTAAGTCCGGC 180

Db 121 CACATCTCTGCCACCTCTGCAGATGTAACGGTCCAGAGGCCCTTCAATCAAGTAAGTCCGGC 180

QY 181 ATCCCGACTACTTCAGCAGATCCCTCCCGAGGGCTTCACTTGGAGCGCACCAACC 240

Db 181 ATCCCGACTACTTCAGCAGATCCCTCCCGAGGGCTTCACTTGGAGCGCACCAACC 240

QY 241 TACGAGGACCGGGGGCTTCTGACCGGCCACAGAGACACTCCCTGAGCGGCGACTGCTG 300

Db 241 TACGAGGACCGGGGGCTTCTGACCGGCCACAGAGACACTCCCTGAGCGGCGACTGCTG 300

QY 301 GTGTACAAAGTGAAGATCTCTGGGCACAACTTCCCGCGACGGGCCCCCGTATGCAGAAC 360

Db 301 GTGTACAAAGTGAAGATCTCTGGGCACAACTTCCCGCGACGGGCCCCCGTATGCAGAAC 360

QY 361 AAGGCGCGCGCTGGGAGGCCCTCCACCGAGATGTGTATAGAGGTGAGACGGCGTGGCGC 420

Db 361 AAGGCGCGCGCTGGGAGGCCCTCCACCGAGATGTGTATAGAGGTGAGACGGCGTGGCGC 420

QY 421 GGCACGTCCAGCATGGCCCTCGAGATGCCCCCGCGGTGCGCACCTGACCTTGACCTTGAC 480

Db 421 GGCACGTCCAGCATGGCCCTCGAGATGCCCCCGCGGTGCGCACCTGACCTTGACCTTGAC 480

QY 481 ACCACTTACCGCTCCAGAGAGCCCGGCTCGGCCCTTAAGATGGCCGGCTTCCACTTCGAG 540

Db 481 ACCACTTACCGCTCCAGAGAGCCCGGCTCGGCCCTTAAGATGGCCGGCTTCCACTTCGAG 540

QY 541 GACCAACCGCATGAGATCTCTGAGGAGATGAGAGAGGCAAGTGTATCAAGCAGTACGAG 600

Db 541 GACCAACCGCATGAGATCTCTGAGGAGATGAGAGAGGCAAGTGTATCAAGCAGTACGAG 600

QY 601 GCGGCGGTGGCGCGCTACTGCGACCGGCCCTCTCAAGTGGGGCCACCAACTGA 654

Db 601 GCGGCGGTGGCGCGCTACTGCGACCGGCCCTCTCAAGTGGGGCCACCAACTGA 654

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RESULT 2
US-10-806-930-7
; Sequence 7, Application US/10806930
; Publication No. US20040216180A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; TITLE OF INVENTION: Nucleic Acids Encoding Linked
; TITLE OF INVENTION: Chromo/Fluorescent Domains and Methods for Using the Same
; FILE REFERENCE: CLON-094
; CURRENT APPLICATION NUMBER: US/10/806, 930
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/976, 673
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/356, 225
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/383, 336
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: PCT/US02/32560
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: anthozoa
US-10-806-930-7

Query Match          99.8%; Score 652.4; DB 18; Length 1404;
Best Local Similarity 99.8%; Pred. No. 1.2e-153;

```

	Matches	65%;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0
QY	1	GAGGACCGTGAACGCGCACTACTTCAAGTGCACCGGCAAGGCGAGGCGCAACCCCTTC								60
Db	46	GAGGGCACCGGTGAACGCGCACTACTTCAAGTGCACCGGCAAGGCGAGGCGCAACCCCTTC								105
QY	61	GAGGGCACCGGAGATGAAGATGAGGATGACGAGGCGGCGCCCTTCGCTTCGCTTC								120
Db	106	GAGGGCACCGGAGATGAAGATGAGGATGACGAGGCGGCGCCCTTCGCTTCGCTTC								165
QY	121	CACATCTGTCCACCTCTCTGACATGTAAGCGCTTCAAGGCTTTCATCAAGTACGTGTCCGCG								180
Db	166	CACATCTGTCCACCTCTCTGACATGTAAGCGCTTCAAGGCTTTCATCAAGTACGTGTCCGCG								225
QY	181	ATCCCGACCTACTTCAAGCACTTCCTCCCGAGGCGCTTCACTTGGAGACCGACCAACCAAC								240
Db	226	ATCCCGACCTACTTCAAGCACTTCCTCCCGAGGCGCTTCACTTGGAGACCGACCAACCAAC								285
QY	241	TACGAGACGCGCGCTTCTGTACGCGCCACCAAGACACCTTCCTTGAACGCGGACCTGCTG								300
Db	286	TACGAGACGCGCGCTTCTGTACGCGCCACCAAGACACCTTCCTTGAACGCGGACCTGCTG								345
QY	301	GTGTCAAGGTGAAGATCTTGGGCAACAATTCCCGCCGACCGGCCCTGTATGACGAAC								360
Db	346	GTGTCAAGGTGAAGATCTTGGGCAACAATTCCCGCCGACCGGCCCTGTATGACGAAC								405
QY	361	AAGGCGGCGCGCTGGAGCCCTTCCACCGAGATCGTACGAGGTGACGCGGTGCGGC								420
Db	406	AAGGCGGCGCGCTGGAGCCCTTCCACCGAGATCGTACGAGGTGACGCGGTGCGGC								465
QY	421	GAGCCATCGACATAGCCCTTGAAGTCCCGCGCGGTGCGCACTTGACCTTGCACTTGCAAC								480
Db	466	GAGCCATCGACATAGCCCTTGAAGTCCCGCGCGGTGCGCACTTGACCTTGCAAC								525
QY	481	AACACCTACCGCTCCAGAAAGCCCGGCTCGGCGCTGAAAGATGCCCGCTTCACTTGCAG								540
Db	526	AACACCTACCGCTCCAGAAAGCCCGGCTCGGCGCTGAAAGATGCCCGCTTCACTTGCAG								585
QY	541	GACCAACCGCATCGAGATCTTGAAGAGGTGAGAAAGGCAAGTGTCAACACAGTACGAG								600
Db	586	GACCAACCGCATCGAGATCTTGAAGAGGTGAGAAAGGCAAGTGTCAACACAGTACGAG								645
QY	601	GCGGCGGTGGCGCGCTACTGACAGCGCGCCCTTCAAGCTTGGGCGCAACTGA								654
Db	646	GCGGCGGTGGCGCGCTACTGACAGCGCGCCCTTCAAGCTTGGGCGCAACTGA								699

RESULT 3
 US-10-006-922-39
 / Sequence 39, Application US/10006922
 / Publication No. US200201976A1
 / GENERAL INFORMATION:
 / APPLICANT: Lukyanov, Sergey A.
 / APPLICANT: Fradkov, Arcady F.
 / APPLICANT: Labas, Yulii A.
 / APPLICANT: Matcz, Mikhail V.
 / APPLICANT: Tersikh, Alexey
 / TITLE OF INVENTION: No. US200201976A1 Chromophores/Fluorophores and
 / TITLE OF INVENTION: Methods for Using the Same
 / FILE REFERENCE: CLON-035C1P
 / CURRENT APPLICATION NUMBER: US/10/006,922
 / CURRENT FILING DATE: 2001-12-04
 / PRIOR APPLICATION NUMBER: 09/1220,330
 / PRIOR FILING DATE: 1998-12-11
 / PRIOR APPLICATION NUMBER: 09/457,898
 / PRIOR FILING DATE: 1999-12-09
 / PRIOR APPLICATION NUMBER: 09/458,144
 / PRIOR FILING DATE: 1999-12-09
 / PRIOR APPLICATION NUMBER: 09/458,477
 / PRIOR FILING DATE: 1999-12-09
 / PRIOR APPLICATION NUMBER: 09/457,556
 / PRIOR FILING DATE: 1999-12-09
 / PRIOR APPLICATION NUMBER: 09/444,338


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; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: non-aggregating mutant
US-10-081-864-21

Query Match      99.3%; Score 649.2; DB 14; Length 707;
Best Local Similarity 99.5%; Pred. No. 7.3e-153;
Matches 651; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GAGGGACACCGTGAAGGGCACTACTTCAAGTGCACCGGCAAGGGGGAAGGGCAACCCCTTC 60
DB      49  GAGGGACACCGTGAAGGGCACTACTTCAAGTGCACCGGCAAGGGGGAAGGGCAACCCCTTC 108
QY      61  GAGGGACACCGGAGATGATGAGGATGATGAGGCGGCGCCCTTGCCTTC 120
DB      109  GAGGGACACCGGAGATGATGAGGATGATGAGGCGGCGCCCTTGCCTTC 168
QY      121  CACATCTGTCCACCTCTCTGATGATGAGGCTTCAAGGCTTTCATCAAGTACGTGTCCGCG 180
DB      169  CACATCTGTCCACCTCTCTGATGATGAGGCTTCAAGGCTTTCATCAAGTACGTGTCCGCG 228
QY      181  ATCCCGCACTACTTCAAGCATGTCTCTCCCGGAGGCTTCACTTGGGAGGCGACCAACACC 240
DB      229  ATCCCGCACTACTTCAAGCATGTCTCTCCCGGAGGCTTCACTTGGGAGGCGACCAACACC 288
QY      241  TACGAGAGCGGGGCTTCTGACCGCGCACAGACACTCCCTGAGACGGGAGCTGCTG 300
DB      289  TACGAGAGCGGGGCTTCTGACCGCGCACAGACACTCCCTGAGACGGGAGCTGCTG 348
QY      301  GTGTACAAAGTGAAGATCTTGCGCAACAATTCCTCCGCGGACGGCCCGTGAATGCAAGAC 360
DB      349  GTGTACAAAGTGAAGATCTTGCGCAACAATTCCTCCGCGGACGGCCCGTGAATGCAAGAC 408
QY      361  AAGGCGGCGCGTGGGAAGCTTCCACCGAGATCTGTACAGAGTGAAGCGGCTGCTGCGC 420
DB      409  AAGGCGGCGCGTGGGAAGCTTCCACCGAGATCTGTACAGAGTGAAGCGGCTGCTGCGC 468
QY      421  GGCCAGTCCAGATGCGCCCTGAGAGGCGCGCGGCTGCGACCTGACCTGCGACCTGCGAC 480
DB      469  GGCCAGTCCAGATGCGCCCTGAGAGGCGCGCGGCTGCGACCTGACCTGCGACCTGCGAC 528
QY      481  ACCACTACCGCTCCCAAGAGCGCGCTCCGCGCTGAAGATGCCCGCTTCCACTTCGAG 540
DB      529  ACCACTACCGCTCCCAAGAGCGCGCTCCGCGCTGAAGATGCCCGCTTCCACTTCGAG 588
QY      541  GACCAACCGCATCGAGATCTTGAGAGGATGAGAAAGGCAAGTCTTCAAGCATGATCGAG 600
DB      589  GACCAACCGCATCGAGATCTTGAGAGGATGAGAAAGGCAAGTCTTCAAGCATGATCGAG 648
QY      601  GCCGCGGTGGGCGGCTACTGCGAGCGCGCGCCCTCCCAAGCTGGGGCAACAACGA 654
DB      649  GCCGCGGTGGGCGGCTACTGCGAGCGCGCGCCCTCCCAAGCTGGGGCAACAACGA 702

RESULT 5
US-10-806-930-9
; Sequence 9, Application US/10806930
; Publication No. US20040216180A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; TITLE OF INVENTION: Nucleic Acids Encoding Linked
; TITLE OF INVENTION: Chromo/Fluorescent Domains and Methods for Using the Same
; FILE REFERENCE: CLON-094
; CURRENT APPLICATION NUMBER: US/10/806,930

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/ CURRENT FILING DATE: 2004-03-22
/ PRIOR APPLICATION NUMBER: 09/976,673
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/356,225
/ PRIOR FILING DATE: 2002-02-11
/ PRIOR APPLICATION NUMBER: 60/383,336
/ PRIOR FILING DATE: 2002-05-22
/ PRIOR APPLICATION NUMBER: PCT/US02/32560
/ PRIOR FILING DATE: 2002-10-10
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 9
/ LENGTH: 1398
/ TYPE: DNA
/ ORGANISM: Anthozoa
US-10-806-930-9

Query Match      99.0%; Score 647.6; DB 18; Length 1398;
Best Local Similarity 99.4%; Pred. No. 1.8e-152;
Matches 650; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
43 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
61 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
103 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
121 CACATCTGTGCTCACTCTGCAATGATGAGGCTTCAAGGCGCTTCAAGTGCACCGG
163 CACATCTGTGCTCACTCTGCAATGATGAGGCTTCAAGGCGCTTCAAGTGCACCGG
181 ATCCCGACCTTCAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
223 ATCCCGACCTTCAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
241 TACGAGGACCGGCGCTTCTGACCGGCGGCGGCTTCAAGGCGCTTCAAGTGCACCGG
283 TACGAGGACCGGCGCTTCTGACCGGCGGCGGCTTCAAGGCGCTTCAAGTGCACCGG
301 GTGTAAAGGTAAGATCTGTGAGCAAACTTCCCGGCGGCGGCTTCAAGTGCACCGG
343 GTGTAAAGGTAAGATCTGTGAGCAAACTTCCCGGCGGCGGCTTCAAGTGCACCGG
361 AAGGCGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCACCGG
403 AAGGCGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCACCGG
421 GGGCAGTCCGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCAC
463 GGGCAGTCCGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCAC
481 ACCACCTACCGCTTCAAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGTGCAC
523 ACCACCTACCGCTTCAAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGTGCAC
541 GACCAACGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGGCGGCTTCAAG
583 GACCAACGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGGCGGCTTCAAG
601 GCGGCGGCGGCTTGTGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGGCGG
643 GCGGCGGCGGCTTGTGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGGCGG

RESULT 6
US-10-006-922-41
/ Sequence 41, Application US/10006922
/ Publication No. US20020197676A1
/ GENERAL INFORMATION:
/ APPLICANT: Lukyanov, Sergey A.
/ APPLICANT: Fridkov, Arcady F.
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/ APPLICANT: Labas, Yulii A.
/ APPLICANT: Marx, Mikhail V.
/ APPLICANT: Terekhikh, Aleksey
/ TITLE OF INVENTION: No. US20020197676A1e1 Chromophores/Fluorophores and
/ TITLE OF INVENTION: Methods for using the Same
/ FILE REFERENCE: CLON-035CIP
/ CURRENT APPLICATION NUMBER: US/10/006,922
/ PRIOR FILING DATE: 2001-12-04
/ PRIOR APPLICATION NUMBER: 09/120,330
/ PRIOR FILING DATE: 1998-12-11
/ PRIOR APPLICATION NUMBER: 09/457,898
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/458,144
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/458,477
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/457,556
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 09/444,338
/ PRIOR FILING DATE: 1999-11-19
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 41
/ LENGTH: 699
/ TYPE: DNA
/ ORGANISM: Anemonia sulcata
US-10-006-922-41

Query Match      98.0%; Score 641.2; DB 13; Length 699;
Best Local Similarity 98.8%; Pred. No. 7.3e-151;
Matches 646; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

1 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
46 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
61 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
106 GAGGGACCCGTAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
121 CACATCTGTGCTCACTCTGCAATGATGAGGCTTCAAGGCGCTTCAAGTGCACCGG
166 CACATCTGTGCTCACTCTGCAATGATGAGGCTTCAAGGCGCTTCAAGTGCACCGG
181 ATCCCGACCTTCAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
226 ATCCCGACCTTCAAGGCGCACTTCAAGTGCACCGGAAAGGGGCAACCCCTTC
241 TACGAGGACCGGCGCTTCTGACCGGCGGCGGCTTCAAGGCGCTTCAAGTGCACCGG
286 TACGAGGACCGGCGCTTCTGACCGGCGGCGGCTTCAAGGCGCTTCAAGTGCACCGG
301 GTGTAAAGGTAAGATCTGTGAGCAAACTTCCCGGCGGCGGCTTCAAGTGCACCGG
346 GTGTAAAGGTAAGATCTGTGAGCAAACTTCCCGGCGGCGGCTTCAAGTGCACCGG
361 AAGGCGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCACCGG
406 AAGGCGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCACCGG
421 GGGCAGTCCGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCAC
466 GGGCAGTCCGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCGGCTTCAAGTGCAC
481 ACCACCTACCGCTTCAAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGTGCAC
526 ACCACCTACCGCTTCAAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGTGCAC
541 GACCAACGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGGCGGCTTCAAG
586 GACCAACGATGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGGCGGCTTCAAG
601 GCGGCGGCGGCTTGTGAGGCGGCTTGTGAGGCGGCTTCAAGGCGGCTTCAAGGCGG
```

Db 646 GCCGCCGTGGCGGCTACTGTCAGACGCCGCCCTCCAGCTGGGCCAACAATA 699

RESULT 7
US-10-724-178-17
; Sequence 17, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odyssey Thera, Inc.
; APPLICANT: Michnick, Stephen
; APPLICANT: Macdonald, Marlie
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: "KPPI" a mutated variant of kindling fluorescent protein ascp frc
; FEATURE:
; OTHER INFORMATION: m. A. sulcata
; NAME/KEY: CDS
; LOCATION: (1)..(696)
US-10-724-178-17

Query Match 95.4%; Score 623.8; DB 18; Length 696;
Best Local Similarity 97.4%; Pred. No. 1.6e-146;
Matches 634; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 GAGGGGACCGTGAACGGCCCACTTCTTCAAGTGCACGGGCAAGGGGCAACCCCTTC 60
DB 46 GAGGGGACCGTGAACGGCCCACTGCTTCAAGTGCATGGGCAAGGGGCAACCCCTTC 105
QY 61 GAGGGGACCGAGATGAAGATCGAGTGCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120
DB 106 GAGGGGACCGAGATGAAGATCGAGTGCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 165
QY 121 CACATCTGTCACTCTCTGCATGTACGGCTCCAAAGGCTTCAATCAAGTACGTGTCGGG 180
DB 166 CACATCTGTCACTCTCTGCATGTACGGCTCCAAAGGCTTCAATCAAGTACGTGTCGGG 225
QY 181 ATCCCGAGCTACTTCAAGAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACCAACC 240
DB 226 ATCCCGAGCTACTTCAAGAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACCAACC 285
QY 241 TACGAGAGCGGGGGCTTCTGACGGCCCAACAGAACCTCCCTGAGCGGCGACTGCTG 300
DB 286 TACGAGAGCGGGGGCTTCTGACGGCCCAACAGAACCTCCCTGAGCGGCGACTGCTG 345
QY 301 GTGTACAAAGTGAAGATCTCTGGGCAAACTTCCCGCGAGCGGCGGCTGTATGACAGAA 360
DB 346 GTGTACAAAGTGAAGATCTCTGGGTAACAATTCCCGCGAGCGGCGGCTGTATGACAGAA 405
QY 361 AAGGCGGG 420
DB 406 AAGGCGGG 465
QY 421 GGGCAGCTCAGCATGGGCGCTGAGTGCAGCGGCGGCTGCGCACTGACCTGCGAC 480
DB 466 GGGCAGCTCCTGATGGCGCTGAGTGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 525
QY 481 ACCACCTACCGCTCAAGAAAGCCGGCTCGGCTGTAAGATGCGGGCTTCCACTTTCAG 540
DB 526 ACCACCTACCGCTCAAGAAAGCCGGCTCGGCTGTAAGATGCGGGCTTCCACTTTCAG 585

QY 541 GACCAACCGATGAGATCTCTGAGAGGTGAGAAAGGGAAGTCTTCAAGCATACGAG 600
DB 586 GACCAACCGATGAGATCTCTGAGAGGTGAGAAAGGGAAGTCTTCAAGCATACGAG 645

QY 601 GCCGCCGTGGCGGCTACTGTCAGACGCCGCCCTCCAGCTGGGCCAACAAC 651
DB 646 GCCGCCGTGGCGGCTACTGTCAGACGCCGCCCTCCAGCTGGGCCAACAAC 696

RESULT 8
US-10-724-178-1046
; Sequence 1046, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odyssey Thera, Inc.
; APPLICANT: Michnick, Stephen
; APPLICANT: Macdonald, Marlie
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1046
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: modif. frag.; KFP F2A, with Met added @ position 1
; FEATURE:
; OTHER INFORMATION: m. A. sulcata
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION: KFP F2A corresponds to aa residues 37-end of KPPI
US-10-724-178-1046

Query Match 86.6%; Score 566.6; DB 18; Length 591;
Best Local Similarity 97.6%; Pred. No. 3.3e-132;
Matches 575; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 63 GGGGACCGGAGATGAAGATCGAGTGCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 122
DB 3 GGGGACCGGAGATGAAGATCGAGTGCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 62
QY 123 CATCTGTCACTCTCTGCATGTACGGCTCCAAAGGCTTCAATCAAGTACGTGTCGGGCA 182
DB 63 CATCTGTCACTCTCTGCATGTACGGCTCCAAAGGCTTCAATCAAGTACGTGTCGGGCA 122
QY 183 CCCCAGCTACTTCAAGCAAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACCAACTA 242
DB 123 CCCCAGCTACTTCAAGCAAGTCTCTCCCGAGGGCTTCACTGGAGGGGCAACCAACTA 182
QY 243 CGAGAGCGGGGGCTTCTGACGGCCCAACAGAACCTCCCTGAGCGGCGACTGCTG 302
DB 183 CGAGAGCGGGGGCTTCTGACGGCCCAACAGAACCTCCCTGAGCGGCGACTGCTG 242
QY 303 GTTACAAAGTGAAGATCTCTGGGCAAACTTCCCGCGAGCGGCGGCTGTATGACAGAA 362
DB 243 GTTACAAAGTGAAGATCTCTGGGTAACAATTCCCGCGAGCGGCGGCTGTATGACAGAA 302
QY 363 GGGCGGG 422
DB 303 GGGCGGG 362
QY 423 CGAGTTCAGCATGGGCGCTGAGTGCAGCGGCGGCTGCGCACTGACCTGCGAC 482
DB 363 CGAGTTCCTGATGGCGCTGAGTGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 422
QY 483 CACTTACCGCTCAAGAAAGCCGGCTCGGCTGTAAGATGCGGGCTTCCACTTTCAG 542

Accession	Sequence	Position
Db	CACTTACCGCTCCAGAGACCCGCTTCGGCTTGAAGATGCCCGGCTTCCACTTCCAGGA	482
Qy	CCACCGCATCGAGATCTTGAGAGAGTGGAGAGGCAATGCTACAGCAGTACGAGGC	602
Db	CCACCGCATCGAGATCATGAGAGAGTGGAGAGGCAATGCTTACAGCAGTACGAGGC	542
Qy	CGCGTGGGCGCGCTACTGTCGAGCGCGCGCTTCCAGACTGGGCGCACAC	651
Db	CGCGCTGGGCGCGCTACTGTCGAGCGCGCGCTTCCAGACTGGGCGCACAC	591

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RESULT 9
US-10-724-178-1064
; Sequence 1064, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odyssey Thera, Inc.
; APPLICANT: Michnick, Stephen
; APPLICANT: MacDonald, Marlene
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENTATION
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1064
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: modif. frag.; KFP FlF, with position 1 Met removed
; NAME/KEY: CDS
; LOCATION: (1)..(555)
; OTHER INFORMATION: KFP FlF corresponds to aa residues 1-186 of KPPI
US-10-724-178-1064

```

Query Match	74.5%	Score 487.4	DB 18	Length 555
Best Local Similarity	96.9%	Pred. No. 2.2e-112		
Matches 497	Conservative	0	Mismatches 16	Indels 0
				Gaps 0
QY	1	GAGGGCA	CGTGAACGGCCACTTCTTCAAGTGCACCGGCAAGGGGGAAGGGCAACCCCTTC	60
Db	43	GAGGGCA	CCGTGAACGGCCACTGCTTCAAGTGCATCTGGCAAGGGGGAAGGGCAACCCCTTC	102
QY	61	GAGGGCA	CCCAAGAGATGAAGATCGAGTGAATCGAGGGCGGCCCCCTGCTCCCTTC	120
Db	103	GAGGGCA	CCCAAGAGATGAAGATCGAGTGAATCGAGGGCGGCCCCCTGCTCCCTTC	162
QY	121	CACATCTGTCA	CACTCTGCATGTACGGCTTCAAGGGCTTCATCAAGTACGTGTCGAC	180
Db	163	CACATCTGTCA	CACTCTGCATGTACGGCTTCAAGACTTCATCAAGTACGTGTCGAC	222
QY	181	ATCCCGCA	CTTCAAGACAGTCCCTCCCGAGGGCTTCACTCGGAGCGCACCAACC	240
Db	223	ATCCCGCA	CTTCAAGACAGTCCCTCCCGAGGGCTTCACTCGGAGCGCACCAACC	282
QY	241	TACAGAGA	CGGCGGCTTCTGTACCGGCCACACAGGACACTCCCTGTGAAGGGGACGTGGC	300
Db	283	TACAGAGA	CGGCGGCTTCTGTACCGGCCACACAGGACACTCCCTGTGAAGGGGACGTGGC	342
QY	301	GTTGTACA	GAGTGAAGATCTGTGGGCAAACTTCCCGCGGACGGCCCGTGTGCAGAAC	360
Db	343	GTTGTACA	GAGTGAAGATCTGTGGGTAACAATTTCCCGCGGACGGCCCGTGTGTGAGAAC	402
QY	361	AAGCGCGG	CGCTGTGGAGCCTTCCACCGAGATGTGTACGAGTGAACGGCGTGTGCGC	420
Db	403	AAGGTGGC	CCCTGTGGAGCCCGGAACCAAGATCGTGTACGAGTGAACGGCGTGTGCGC	462

QY	421	GGCCAGTCTCAGCAATGGCCCTCGAAGTCCCGGCGGTGCGACCTGACCTGGCAC	480
Db	463	GCCACGTCTTGATGATGCCCTGAAGTCCCCCGGCGCGGACCTGACTGCACTGGCAC	522
QY	481	ACCACTTACCGCTCCAGAGCGCGCGCTTCGGCTC	513
Db	523	ACCACTTACCGCTCCAGAGCGCGCGCTTCGGCTC	555

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RESULT 10
US-10-724-178-1060
; Sequence 1060, Application US/10724178
; Publication No. US20040137528A1
; GENERAL INFORMATION:
; APPLICANT: Odyssey Thera, Inc.
; APPLICANT: Michnick, Stephen
; APPLICANT: Macdonald, Marnie
; APPLICANT: Lamerdin, Jane
; TITLE OF INVENTION: FRAGMENTS OF FLUORESCENT PROTEINS FOR PROTEIN-FRAGMENT
; FILE REFERENCE: ODDY007
; CURRENT APPLICATION NUMBER: US/10/724,178
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: US 60/461,133
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1060
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: modif. frag.; KFP F1B, with position 1 Met removed
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(504)
; OTHER INFORMATION: KFP F1B corresponds to aa residues 1-169 of KPFI
US-10-724-178-1060

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[illegible]

Db 463 GGGCACTCCCTGATGCGCTTGAAGTGCCTCCCGCGCGGCGAC 504

RESULT 11

US-10-006-922-13
Sequence 13, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey A.
APPLICANT: Fradkov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terelikh, Alexey
TITLE OF INVENTION: No. US20020197676A1 Chromophores/Fluorophores and
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/458,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/457,556
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/444,338
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 696
TYPE: DNA
ORGANISM: Anemonia sulcata
US-10-006-922-13

Query Match 63.6%; Score 415.8; DB 13; Length 696;
Best Local Similarity 77.4%; Pred. No. 1.7e-94;
Matches 504; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 60
DB 46 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 105
QY 61 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 120
DB 106 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 165
QY 121 CACATCTGTCACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 166 CACATCTGTCACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 225
QY 181 ATCCCGACTTCTTCAAGAGTCCCTCCCGAGGGCTTCACTGAGGCGACCAAC 240
DB 226 ATCCCGACTTCTTCAAGAGTCCCTCCCGAGGGCTTCACTGAGGCGACCAAC 285
QY 241 TACGAGAGCGGGCTTCTGACCGCGCACAGAGACCTTCTGAGCGGAGCTGCTG 300
DB 286 TACGAGAGCGGGCTTCTGACCGCGCACAGAGACCTTCTGAGCGGAGCTGCTG 345
QY 301 GTGTACAAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGCCCTGATGAGAAC 360
DB 346 GTTACAAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGCCCTGATGAGAAC 405
QY 361 AAGGCGCGCGCTGAGAGCGCTTCAAGAGTGTGATGAGAGTGAAGCGGCTGCGC 420
DB 406 AAGGCGCGCGCTGAGAGCGCTTCAAGAGTGTGATGAGAGTGAAGCGGCTGCGC 465
QY 421 GGGCACTCCAGATGCGCCCTGAGAGTGCCTCCCGCGGCTGCGCACTGAGCTGCGAC 480

Db 466 GGAAGTCTTTGATGCGCCCTTAAGTGCCTGATGATGATGATGATGATGATGATGAT 525
QY 481 ACCACTTACCGTCCAGAGAGCGCCCTTCCGCTTGAAGATGCGGCTTCACTTCCAG 540
DB 526 ACTACTTACAGGTCCAAAACACACCTGCTGCTTGAAGATGCGGATTTCACTTTGAA 585
QY 541 GACCAACCGCATGAGATCCTGAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
DB 586 GATCATGCGATGAGATTAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 645
QY 601 GCGCGCGTGGCGGCTACTGCGAGCGCGCCCTTCAAGCTGGGCGACAAAC 651
DB 646 GCAGAGTGGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696

RESULT 12

US-10-081-864-9
Sequence 9, Application US/10081864
Publication No. US20030022287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
APPLICANT: Konstantin
APPLICANT: Yanushevich, Yuriy
APPLICANT: Savitsky, Alexandr
APPLICANT: Fradkov, Arcady
TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
FILE REFERENCE: CLON-067
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/270,983
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 696
TYPE: DNA
ORGANISM: Anemonia sulcata
US-10-081-864-9

Query Match 63.6%; Score 415.8; DB 14; Length 696;
Best Local Similarity 77.4%; Pred. No. 1.7e-94;
Matches 504; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 60
DB 46 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 105
QY 61 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 120
DB 106 GAGGGCACTGTAAGCGCCACTTCTCAAGTGCACCGGCGAGGGCAACCCCTTC 165
QY 121 CACATCTGTCACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 166 CACATCTGTCACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 225
QY 181 ATCCCGACTTCTTCAAGAGTCCCTCCCGAGGGCTTCACTGAGGCGACCAAC 240
DB 226 ATCCCGACTTCTTCAAGAGTCCCTCCCGAGGGCTTCACTGAGGCGACCAAC 285
QY 241 TACGAGAGCGGGCTTCTGACCGCGCACAGAGACCTTCTGAGCGGAGCTGCTG 300
DB 286 TACGAGAGCGGGCTTCTGACCGCGCACAGAGACCTTCTGAGCGGAGCTGCTG 345
QY 301 GTGTACAAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGCCCTGATGAGAAC 360
DB 346 GTTACAAGGTGAAGATCTCTGGGCAACACTTCCCGCGAGCGCCCTGATGAGAAC 405
QY 361 AAGGCGCGCGCTGAGAGCGCTTCAAGAGTGTGATGAGAGTGAAGCGGCTGCGC 420
DB 406 AAGGCGCGCGCTGAGAGCGCTTCAAGAGTGTGATGAGAGTGAAGCGGCTGCGC 465


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Db      294 ATTCTGACTTACTTCAAGAGTCTTTCCCTGAGAGTTTACTTGGAGAAAGACCAAC 353
Qy      241 TACGAGAGCGGCGCTTCTCTGACCGGCCACAGAGACCTCCCTGAGCGGCACTGCG 300
Db      354 TACGAGAGTGAAGGCTTTCTTACAGCTCATACAGGACCAAGCTTAGATGAGATTGCTTC 413
Qy      301 GTGTACAGAGTGAAGTCTTGGGCAACAATTCCCGCCGACGCGCCCTGTATGCGAAG 360
Db      414 GTTTACAAAGTCAAGATTCTTGTATATATTTTCTGCTGATGCGCCCTGTAGCAGAAC 473
Qy      361 AAGGCGGCGCGCTGGAGGCGCTCCACCGAGATCGTGTACAGAGTGAAGCGGCGTGGCC 420
Db      474 AAGGAGGAGATGGAGAGCCAGGACCGAGATGTTATGAGATTACCGGTCTGCGT 533
Qy      421 GGCAGATCCAGATGCGCCCTGAGTCCCGCGGCGTCCGCACTGCACTGCAAC 480
Db      534 GGACAGTCTTTGATGAGCCCTTAAGTCCCTGAGTGTGTCATCTGACTTGGCATCTCCAT 593
Qy      481 ACCACTTACCGCTCCAGAGAGCGCGCTCCGCTGAAATGCGCGCTTCCACTTCGAG 540
Db      594 ACTACTTACAGGTCGCAAAAAACAGAGTGTGCTTGAAGATGCGAGATTTCATTTTGA 653
Qy      541 GACCAACCGATCGAGATCCGTGAGAGGTGAGAGAGGCAAGTGTACAGAGTACGAG 600
Db      654 GATCATCGCATCGAGATTAATGAGAGAGTTGAGAGAGGCAAGTGTATTAACAGTACGA 713
Qy      601 GCCGCGGTGGCGCGCTACTGCGAGCGCGCCCTCCAACTGGGCCCAACTGA 654
Db      714 GCAGAGTGGGAGGTACTGTGATGCTGCTCCATCCAACTGGAATTAATA 767

RESULT 15
US-10-155-809-5
; Sequence 5, Application US/10155809
; Publication No. US20030092884A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Chudakov, Dmitry
; TITLE OF INVENTION: Kindling Fluorescent Proteins and
; FILE REFERENCE: CLON-073
; CURRENT APPLICATION NUMBER: US/10/155,809
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,752
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/329,176
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/210,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/976,673
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 767
; TYPE: DNA
; ORGANISM: anthozoa
US-10-155-809-5

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Query Match 62.6%; Score 409.2; DB 14; Length 767;
 Best Local Similarity 76.6%; Pred. No. 7.8e-93;
 Matches 501; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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Qy      1  GAGGGACCGTGAACCGCACTTCAAGTGAACCGGAGGAGGCAACCCCTTC 60
Db      114 GAAGGAGCGGTATAGCCACTTCAAGTGAACGAGAAAGAGGAGGCAACCAATT 173
Qy      61  GAGGGACCGCAGAGATGAAGATCGAGTATGAGGCGGCGCCCTGCGCTTC 120

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Db      174 GAGGGTACGAGAAATGAATGATAGAGTCAATGAGAGGATCAATTTGCTTC 233
Qy      121 CACATCTGTCCACTCTCTGCAATGTAAGGCTCCAGGCTTCAATCAAGTGTCTCGGC 180
Db      234 CACATTTGTCAACGAGTGTATGTAAGTATGAGACCTTCAATCAAGTATGTCTCAGA 293
Qy      181 ATCCCGACTACTTCAAGAGTCCCTCCCGAGGAGGCTTCACTGGAGGCGCACACACC 240
Db      294 ATTCTGACTTACTTCAAGAGTCTTTCCCTGAGAGTCTTACTTGGAGAAAGACCAAC 353
Qy      241 TACGAGAGCGGCGCTTCTCTGACCGGCCACAGAGACCTCCCTGAGCGGCACTGCG 300
Db      354 TACGAGAGTGAAGGCTTTCTTACAGCTCATACAGGACCAAGCTTAGATGAGATTGCTTC 413
Qy      301 GTGTACAGAGTGAAGTCTTGGGCAACAATTCCCGCCGACGCGCCCTGTATGCGAAG 360
Db      414 GTTTACAAAGTCAAGATTCTTGTATATATTTTCTGCTGATGCGCCCTGTATGCGAAG 473
Qy      361 AAGGCGGCGCGCTGGAGGCGCTCCACCGAGATCGTGTACAGAGTGAAGCGGCGTGGCC 420
Db      474 AAGGAGGAGATGGAGAGCCAGGACCGAGATGTTATGAGATTACCGGTCTGCGT 533
Qy      421 GGCAGATCCAGATGCGCCCTGAGTCCCGCGGCGTCCGCACTGCACTGCAAC 480
Db      534 GGACAGTCTTTGATGAGCCCTTAAGTCCCTGAGTGTGTCATCTGACTTGGCATCTCCAT 593
Qy      481 ACCACTTACCGCTCCAGAGAGCGCGCTCCGCTGAAATGCGCGCTTCCACTTCGAG 540
Db      594 ACTACTTACAGGTCGCAAAAAACAGAGTGTGCTTGAAGATGCGAGATTTCATTTTGA 653
Qy      541 GACCAACCGATCGAGATCCGTGAGAGGTGAGAGAGGCAAGTGTACAGAGTACGAG 600
Db      654 GATTAACCGCATCGAGATTAATGAGAGAGTTGAGAGAGGCAAGTGTATTAACAGTACGA 713
Qy      601 GCCGCGGTGGCGCGCTACTGCGAGCGCGCCCTCCAACTGGGCCCAACTGA 654
Db      714 GCAGAGTGGGAGGTACTGTGATGCTGCTCCATCCAACTGGAATTAATA 767

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 Job time : 529.342 secs

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